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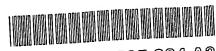
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(S) Imidazolinone resistant ahas mutants.

The present invention relates to monocot genes encoding a mutant AHAS enzyme that is specifically resistant to imidazolinone herbicides. Exemplary of these genes are corn DNA sequences which encode an amino acid substitution at position 621 of the wild-type AHAS enzyme. The mutant gene can be used to amino acid substitution at position 621 of the wild-type AHAS enzyme. The mutant gene can be used to transform other plants to herbicide resistance; in this regard, the invention also provides host cells and vectors containing the gene, which cells and vectors are useful in the transformation process.

This invention relates to novel DNA sequences that encode novel variant forms of acetohydroxy acid synthase enzyme (hereinafter AHAS). The AHAS enzyme is a critical enzyme routinely produced in a variety of plants and a broad range of microorganisms. Normal AHAS function is inhibited by imidazolinone herbicides; however, new AHAS enzymes encoded by the mutant DNA sequences function normally catalytically even in the presence of imidazolinone herbicides and, therefore, confer herbicide resistance upon the plant or microorganism containing them.

The novel DNA sequences are derived from corn and have a substitution of an amino acid at position 621 of the normal AHAS sequence. This substitution in the AHAS gene sequence results in a fully functional enzyme, but renders the enzyme specifically resistant to inhibition by a variety of imidazolinone herbicides. The availability of these variant sequences provides a tool for transformation of different crop plants to imidazolinone herbicide resistance, as well as providing novel selectable markers for use in other types of genetic transformation experiments.

BACKGROUND OF THE INVENTION

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The use of herbicides in agriculture is now widespread. Although there are a large number of available compounds which effectively destroy weeds, not all herbicides are capable of selectively targeting the undersirable plants over crop plants, as well as being non-toxic to animals. Often, it is necessary to settle for compounds which are simply less toxic to crop plants than to weeds. In order to overcome this problem, development of herbicide resistant crop plants has become a major focus of agricultural research.

An important aspect of development of herbicide-resistance is an understanding of the herbicide target, and then manipulating the affected biochemical pathway in the crop plant so that the inhibitory effect is avoided while the plant retains normal biological function. One of the first discoveries of the biochemical mechanism of herbicides related to a series of structurally unrelated herbicide compounds, the imidazolinones, the sulfonylureas and the triazolopyrimidines. It is now known (Shaner et al. Plant Physiol. 76: 545-546,1984; U.S. Patent No. 4,761,373) that each of these herbicides inhibits plant growth by interference with an essential enzyme required for plant growth, acetohydroxyacid synthase (AHAS; also referred to as acetolacetate synthase, or ALS). AHAS is required for the synthesis of the amino acids isoleucine, leucine and valine.

The AHAS enzyme is known to be present throughout higher plants, as well as being found in a variety of microorganisms, such as the yeast Saccharomyces cerevisiae, and the enteric bacteria, Escherichia coli and Salmonella typhimurium. The genetic basis for the production of normal AHAS in a number of these species has also been well characterized. For example, in both E. coli and S. typhimurium three isozymes of AHAS exist; two of these are sensitive to herbicides while a third is not. Each of these isozymes possesses one large and one small protein subunit; and map to the IIvIH, IIvGM and IIvBN operons. In yeast, the single AHAS isozyme has been mapped to the ILV2 locus. In each case, sensitive and resistant forms have been identified and sequences of the various alleles have been determined (Friden et. al., Nucl. Acid Res. 13: 3979-3993, 1985; Lawther et al., PNAS USA 78: 922-928, 1982; Squires et al., Nucl. Acids Res 811: 5299-5313, 1983; Wek et al; Nucl. Acids Res 13: 4011-4027, 1985; Falco and Dumas, Genetics 109, 21-35, 985; Falco et al, Nucl. Acids Res 13; 4011-4027, 1985).

In tobacco, AHAS function is encoded by two unlinked genes, SuRA and SuRB. There is substantial identity between the two genes, both at the nucleotide level and amino acid level in the mature protein, although the N-terminal, putative transit region differs more substantially (Lee et al, EMBO J. 7: 1241-1248, 1988). Arabidopsis, on the other hand, has a single AHAS gene, which has also been completely sequenced (Mazur et al., Plant Physiol. 85:1110-1117, 1987). Comparisons among sequences of the AHAS genes in higher plants indicates a high level of conservation of certain regions of the sequence; specifically, there are at least 10 regions of sequence conservation. It has previously been assumed that these conserved regions are critical to the function of the enzyme, and that retention of that function is dependent upon substantial sequence conservation.

It has been recently reported (U.S. Patent No. 5,013,659) that mutants exhibiting herbicide resistance possess mutations in at least one amino acid in one or more of these conserved regions. In particular, substitution of certain amino acids for the wild type amino acid at these specific sites in the AHAS protein sequence have been shown to be tolerated, and indeed result in herbicide resistance of the plant possessing this mutation, while retaining catalytic function. The mutations described therein encode either cross resistance for imidazolinones and sulfonylureas or sulfonylurea-specific resistance, but no imidazolinone-specific mutations were disclosed. These mutations have been shown to occur at both the SuRA and SuRB loci in tobacco; similar mutations have been isolated in Arabidopsis and yeast.

Imidazolinone-specific resistance has been reported elsewhere in a number of plants. U.S. Patent No.

4,761,373 generally described an altered AHAS as a basis of herbicide resistance in plants, and specifically disclosed certain imidazolinone resistant corn lines. Haughn et al. (Mol. Gen. Genet. 211:266-271, 1988) disclosed the occurrence of a similar phenotype in Arabidopsis. Sathasivan et al. (Nucl. Acid Res. 18:2188, 1990) identified the imidazolinone-specific resistance in Arabidopsis as being based on a mutation at position 653 in the normal AHAS sequence. In accordance with the present invention, a gene encoding imidazolinone-specific resistance in a monocot has now been isolated and determined to be associated with a single amino acid substitution in a wild-type monocot AHAS amino acid sequence.

SUMMARY OF THE INVENTION

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The present invention provides novel nucleic acid sequences encoding functional monocot AHAS enzymes insensitive to imidazolinone herbicides. The sequences in question comprise a mutation in the codon encoding the amino acid serine at position 621 in the corn (maize) AHAS sequence, or in the corresponding position in other monocot sequences. Other monocots, such as wheat, are also known to exhibit imidazolinone specific mutations (e.g., ATCC Nos. 40994-97). In corn, the wild type sequence has a serine at this position. In a preferred embodiment, the substitution is asparagine for serine, but alternate substitutions for serine include aspartic acid, glutamic acid, glutamine and tryptophane. Although the claimed sequences are originally derived from monocots, the novel sequences are useful in methods for producing imidazolinone resistant cells in any type of plant, said methods comprising transforming a target plant cell with one or more of the altered sequences provided herein. Alternatively, mutagenesis is utilized to create mutants in plant cells or seeds containing a nucleic acid sequence encoding an imidazolinone insensitive AHAS. In the case of mutant plant cells isolated in tissue culture, plants which possess the imidazolinone resistant or insensitive trait are then regenerated. The invention thus also encompasses plant cells, bacterial cells, fungal cells, plant tissue cultures, adult plants, and plant seeds that possess a mutant nucleic acid sequence and which express functional imidazolinone resistant AHAS enzymes.

The availability of these novel herbicide resistant plants enables new methods of growing crop plants in the presence of imidazolinones. Instead of growing non-resistant plants, fields may be planted with the resistant plants produced by mutation or by transformation with the mutant sequences of the present invention, and the field routinely treated with imidazolinones, with no resulting damage to crop plants.

The mutant nucleic acids of the present invention also provide novel selectable markers for use in transformation experiments. The nucleic acid sequence encoding a resistant AHAS is linked to a second gene prior to transfer to a host cell, and the entire construct transformed into the host. Putative transformed cells are then grown in culture in the presence of inhibitory amounts of herbicide; surviving cells will have a high probability of having successfully acquired the second gene of interest. Alternately, the resistant AHAS gene can be cotransformed on an independent plasmid with the gene of interest, whereby about 50% of all transformants can be expected to have received both genes.

The following definitions should be understood to apply throughout the specification and claims. A "functional" or "normal" AHAS enzyme is one which is capable of catalyzing the first step in the pathway for synthesis of the essential amino acids isoleucine, leucine and valine. A "wild-type" AHAS sequence is a sequence present in an imidazolinone sensitive member of a given species. A "resistant" plant is one which produces a mutant but functional AHAS enzyme, and which is capable of reaching maturity when grown in the presence of normally inhibitory levels of imidazolinone. The term "resistant", as used herein, is also intended to encompass "tolerant" plants, i.e., those plants which phenotypically evidence adverse, but not lethal, reactions to the imidazolinone.

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BRIEF DESCRIPTION OF THE FIGURES

Figure 1: AHAS enzyme activity in 10-day old maize seedlings (corn lines A619 or XI12) in the presence of imazethapyr (Pursuit™ A) or chlorsulfuron (Oust™ B). Herbicide resistant AHAS activity is calculated as percentage of AHAS activity in the absence of inhibitor. The standard error between experimets is 10%.

Figure 2: Southern analysis of genomic clones in phage EMBL3. Phages 12-1A (from W22), 12-7A, 18-8A, 12-11, and 12-17A (From XI12) are digested with Xbal or Sall, separated on a 1% agarose gel, transfered onto nitrocellulose and hybridized with an AHAS cDNA fragment as probe.

Figure 3: Southern analysis of genomic DNA from corn lines XI12, XA17, QJ22, A188 and B73. The DNA is digested with Xbal, separated on a 1% agarose gel, transferred onto nitrocellulose and hybridized with an AHAS cDNA fragment as probe.

Figure 4: Restriction map of plasmid pCD8A. The mutant AHAS gene from XI12 was subcloned as a

8kb Pstl fragment into vector pKS(+). The location and orientation of the AHAS gene is indicated by an arrow. The restriction sites of Pstl, Xhol, HindIII, Xbal and Clal are represented by symbols.

Figure 5: Nucleotide sequencing gel of the non-coding strand (A) and the double stranded DNA sequence (B) of AHAS clones W22/4-4, B73/10-4 and XI12/8A in the region of amino acids 614 to 633. The position of the cytosine to thymidine transition is indicated by an arrow.

Figure 6: Nucleotide and deduced amino acid sequences of the XI12/8A mutant AHAS gene.

Figure 7: Nucleotide sequence alignment of XI12/8A, B73/7-4 and W22/1A als2 genes. (*) marks the base change causing the mutation at position 621, (#) differences from the B73/7-4 sequence and (>) represents silent changes.

Figure 8: Amino acid sequences and alignment of XI12/BA, B73/7-4 and W22/1A als2 genes. (*) marks the mutation at position 621, (#) marks differences from the B73/7-4 sequence, and (>) represents silent changes.

DETAILED DESCRIPTION OF THE INVENTION

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The gene of the present invention is isolatable from corn maize line XI12 (seed deposited with the American Type Culture Collection as Accession Number 75051), and has been inserted into plasmid pXI12/8A (deposited with the American Type Culture Collection as Accession Number 68643). It is also isolatable from any other imidazolinone-specific herbicide resistant mutant, such as the corn line QJ22 (deposited as a cell culture with the American Type Culture Collection as Accession Number 40129), or the various wheat plants (seed deposited with the American Type Collection as Accession Numbers 40994, 40995, 40996, or 40997). A genomic DNA library is created, for example, in phage ENBL-3 with DNA from one of the imidazolinone resistant mutants, preferably one which is homozygous for the resistance trait, and is screened with a nucleic acid probe comprising all or a part of a wild-type AHAS sequence.

In maize, the AHAS gene is found at two loci, als1 and als2 (Burr and Burr, Trends in Genetics 7:55-61, 1991); the homology between the two loci is 95% at the nucleotide level. The mutation in XI12 is mapped to locus als2 on chromosome 5, whereas the nonmutant gene is mapped to locus als1 on chromosome 4 (Newhouse et al., "Imidazolinone-resistant crops". In The Imidazolinone Herbicides, Shaner and O'Connor (Eds.), CRC Press, Boca Raton, FL, in Press) Southern analysis identifies some clones containing the mutant als2 gene, and some containing the non-mutant als1 gene. Both types are subcloned into sequencing vectors, and sequenced by the dideoxy sequencing method.

Sequencing and comparison of wild type and mutant AHAS genes shows a difference of a single nucleotide in the codon encoding the amino acid at position 621 (Figure 5). Specifically, the codon AGT encoding serine in the wild type is changed to AAT encoding asparagine in the mutant AHAS (Figure 8). The mutant AHAS gene is otherwise similar to the wild type gene, encoding a protein having 638 amino acids, the first 40 of which constitute a transit peptide which is thought to be cleaved during transport into the chloroplast in vivo. The sequence of the als1 non-mutant gene from XI12 appears to be identical to the als1 gene from B73.

The mutant genes of the present invention confer resistance to imidazolinone herbicides, but not to sulfonylurea herbicides. Types of herbicides to which resistance is conferred are described for example in U.S. Patent Nos. 4,188,487; 4,201,565; 4,221,586; 4,297,128; 4,554,013; 4,608,079; 4,638,068; 4,747,301; 4,650,514; 4,698,092; 4,701,208; 4,709,036; 4,752,323; 4,772,311; and 4,798,619.

It will be understood by those skilled in the art that the nucleic acid sequence depicted in Figure 6 is not the only sequence which can be used to confer imidazolinone-specific resistance. Also contemplated are those nucleic acid sequences which encode an identical protein but which, because of the degeneracy of the genetic code, possess a different nucleotide sequence. The invention also encompasses genes encoding AHAS sequences in which the aforestated mutation is present, but which also encode one or more silent amino acid changes in portions of the molecule not involved with resistance or catalytic function. Also contemplated are gene sequences from other imidazolinone resistant monocots which have a mutation in the corresponding region of the sequences.

For example, alterations in the gene sequence which result in the production of a chemically equivalent amino acid at a given site are contemplated; thus, a codon for the amino acid alanine, a hydrophobic amino acid, can readily be substituted by a codon encoding another hydrophobic residue, such as glycine, or may be substituted with a more hydrophobic residue such as valine, leucine, or isoleucine. Similarly, changes which result in substitution of one negatively charged residue for another, such as aspartic acid for glutamic acid, or one positively charged residue for another, such as lysine for arginine, can also be expected to produce a biologically equivalent product. The invention also encompasses chimaeric genes, in which the substituted portion of the corn AHAS gene is recombined with unaltered portions of the normal AHAS genes

from other species. Thus, throughout the specification and claims, wherever the term "imidazolinone-specific resistant corn AHAS gene" is used, it is intended to cover each of these alternate embodiments as well as the sequence of Figure 6.

Isolated AHAS DNA sequences of the present invention are useful to transform target crop plants, and thereby confer imidazolinone resistance. A broad range of techniques currently exist for achieving direct or indirect transformation of higher plants with exogenous DNA, and any method by which the novel sequence can be incorporated into the host genome, and stably inherited by its progeny, is contemplated by the present invention. The imidazolinone specific resistance trait is inherited as a single dominant nuclear gene. The level of imidazolinone resistance is increased when the gene is present in a homozygous state; such corn plants, for example, have a resistance level of about 1,000 times that of a non-resistant plant. Plants heterozygous for the trait, however, have a resistance of about 50-500 times that of a non-resistant plant.

Transformation of plant cells can be mediated by the use of vectors. A common method of achieving transformation is the use of Agrobacterium tumefaciens to introduce a foreign gene into the target plant cell. For example, the mutant AHAS sequence is inserted into a plasmid vector containing the flanking sequences in the Ti-plasmid T-DNA. The plasmid is then transformed into E. coli. A triparental mating among this strain, an Agrobacterium strain containing a disarmed Ti-plasmid containing the virulence functions needed to effect transfer of the AHAS containing T-DNA sequences into the target plant chromosome, and a second E. coli strain containing a plasmid having sequences necessary to mobilize transfer of the AHAS construct from E. coli to Agrobacterium is carried out. A recombinant Agrobacterium strain, containing the necessary sequences for plant transformation is used to infect leaf discs. Discs are grown on selection media and successfully transformed regenerants are identified. The recovered plants are resistant to the effects of herbicide when grown in its presence. Plant viruses also provide a possible means for transfer of exogenous DNA.

Direct uptake of plant cells can also be employed. Typically, protoplasts of the target plant are placed in culture in the presence of the DNA to be transferred, and an agent which promotes the uptake of DNA by protoplast. Useful agents in this regard are polyethylene glycol or calcium phosphate.

Alternatively, DNA uptake can be stimulated by electroporation. In this method, an electrical pulse is used to open temporary pores in a protoplast cell membrane, and DNA in the surrounding solution is then drawn into the cell through the pores. Similarly, microinjection can be employed to deliver the DNA directly into a cell, and preferably directly into the nucleus of the cell.

In each of the foregoing techniques, transformation occurs in a plant cell in culture. Subsequent to the transformation event, plant cells must be regenerated to whole plants. Techniques for the regeneration of mature plants from callus or protoplast culture are now well known for a large number of different species (see, e.g., Handbook of Plant Cell Culture, Vols. 1-5, 1983-1989 McMillan, N.Y.) Thus, once transformation has been achieved, it is within the knowledge in the art to regenerate mature plants from the transformed plant cells.

Alternate methods are also now available which do not necessarily require the use of isolated cells, and therefore, plant regeneration techniques, to achieve transformation. These are generally referred to as "ballistic" or "particle acceleration" methods, in which DNA coated metal particles are propelled into plant cells by either a gunpowder charge (Klein et al., Nature 327: 70-73, 1987) or electrical discharge (EPO 270 356). In this manner, plant cells in culture or plant reproductive organs or cells, e.g. pollen, can be stably transformed with the DNA sequence of interest.

In certain dicots and monocots direct uptake of DNA is the preferred method of transformation. For example, in corn, the cell wall of cultured cells is digested in a buffer with one or more cell wall degrading enzymes, such as cellulase, hemicellulase and pectinase, to isolate viable protoplasts. The protoplasts are washed several times to remove the enzymes, and mixed with a plasmid vector containing the gene of interest. The cells can be transformed with either PEG (e.g. 20% PEG 4000) or by electroporation. The protoplasts are placed on a nitrocellulose filter and cultured on a medium with embedded corn cells functioning as feeder cultures. After 2-4 weeks, the cultures in the nitrocellulose filter are placed on a medium containing about $0.32~\mu M$ of the imidazolinone and maintained in the medium for 1-2 months. The nitrocellulose filters with the plant cells are transferred to fresh medium with herbicides and nurse cells every two weeks. The untransformed cells cease growing and die after a few weeks.

The present invention can be applied to transformation of virtually any type of plant, both monocot and dicot. Among the crop plants for which transformation to herbicide resistance is contemplated are corn, wheat, rice, millet, oat, barley, sorghum, sunflower, sweet potato, alfalfa, sugar beet, Brassica species, tomato, pepper, soybean, tobacco, melon, squash, potato, peanut, pea, cotton, or cacao. The novel sequences may also be used to transform ornamental species, such as rose, and woody species, such as pine and poplar.

The novel sequences of the invention also are useful as selectable markers in plant genetics studies. For example, in plant transformation, sequences encoding imidazolinone resistance could be linked to a gene of interest which is to be used to transform a target imidazolinone sensitive plant cell. The construct comprising both the gene of interest and the imidazolinone resistant sequence are introduced into the plant cell, and the plant cells are then grown in the presence of an inhibitory amount of an imidazolinone. Alternately, the second gene of interest can be cotransformed, on a separate plasmid, into the host cells. Plant cells surviving such treatment presumably have acquired the resistance gene as well as the gene of interest, and therefore, only transformants survive the selection process with the herbicide. Confirmation of successful transformation and expression of both genes can be achieved by Southern hybridization of genomic DNA, by PCR or by observation of the phenotypic expression of the genes.

The invention is further illustrated by the following non-limiting examples.

EXAMPLES

1. Confirmation of Whole Plant Herbicide Resistance in XI12

XI12 plants are treated with herbicides at 10 days to the V3 leaf stage (4-5 leaves, of which 3 have visible ligules). Imazethapyr is applied at rates of 2000, 500, 250, 125 and 62.5 g/ha. Chlorsulfuron is applied at 32, 16, 8, 4 and 2 g/ha. Plants are treated postemergence at a spray volume of 400 l/ha. After spraying, plants are placed in the greenhouse for further observation.

XI12 plants are unaffected at all rates of imazethapyr treatment; however, no visible increased resistance to chlorsulfuron is noted. Thus, XI12 displays selective resistance to the imidazolinone at the whole plant level (See Figure 1).

The resistance in XI12 is also shown to be inherited as a single dominant allele of a nuclear gene. Heterozygous resistant XI12 are selfed, and the selfed progeny segregate in the 3 resistant:1 susceptible ratio expected for a single dominant allele of a nuclear gene. In this study, the segregating seedlings are sprayed postemergence with lethal doses of imazethapyr (125 or 250 g/ha) following spraying protocols described above, to establish segregation for resistance.

o 2. AHAS Extraction

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Seeds of XI12 are sown in soil in a greenhouse maintained at day/night temperature of 80°C and 15 hour photoperiod. Plants are harvested two weeks after planting. The basal portion of the shoot is used for the extraction of AHAS. 5 g of the tissue is powdered in liquid nitrogen and then homogenized in AHAS assay buffer comprising 100 mM potassium phosphate buffer (pH 7.5) containing 10 mM pyruvate, 5 mM MgCl₂, 5 mM EDTA, 100 uM FAD (flavin adenine dinucleotide), 1 mM valine, 1 mM leucine, 10% glycerol and 10 mM cysteine. The homogenate is centrifuged at 10,000 rpm for 10 minutes and 3 ml of the supernatant are applied onto an equilibrated Bio-Rad Econo-Desalting column (10 DG) and eluted with 4 ml AHAS assay buffer.

AHAS activity is measured by estimation of the product, acetolactate, after conversion by decarbox-ylation in the presence of acid to acetoin. Standard reaction mixtures contain the enzyme in 50 mM potassium phosphate (pH 7.0) containing 100 mM sodium pyruvate, 10 mM MgCl₂, 1 mM thiamine pyrophosphate, 10 uM FAD, and appropriate concentrations of different inhibitors. This mixture is incubated at 37°C for 1 to 3 hours depending upon the experiment. At the end of this incubation period, the reaction is stopped with the addition of H₂SO₄ to make a final concentration of 0.85% H₂SO₄ in the tube. The reaction product is allowed to decarboxylate at 60°C for 15 minutes. The acetoin formed is determined by incubating with creatine (0.17%) and 1-naphthol (1.7% in 4N NaOH). The absorption of color complex formed is measured at 520 nm.

AHAS activity from B73, A619, or other wild-type maize lines is highly sensitive to inhibition by imazethapyr (PURSUITTM) with an I_{50} of 1 uM (See Figure 1). Contrary to this observation, XI12 shows 70-80% of enzyme activity at the highest concentrations (100 μ M) of PURSUITTM or ARSENALTM (imazepyr), and about 70% in the presence of SCEPTERTM (imazequin). This result shows a 100-fold increase in tolerance of AHAS activity from XI12 to imazethapyr as compared to the in vitro AHAS activity from A619. sensitivity of AHAS activity from the two lines to sulfonylureas gives a different picture. In the presence of OUSTTM (sulfometuron methyl), at 100 nM, AHAS activity of XI12 is only 15-20%. AHAS activity of A619 in the presence of OUSTTM IS 5-10%, and in the presence of PURSUITTM is 15-20% (See Figure 1).

3. Cloning of XI12 AHAS Genes

Seeds of the XI12 mutant derived from an imidazolinone resistant corn tissue culture line are planted; plants obtained therefrom appear to be segregating for the mutant AHAS phenotype. In order to obtain homozygous resistant seed material, a population of XI12 mutant plants are selfed. After selecting for herbicide resistance for three consecutive growing seasons, the seeds are homozygous for the mutant AHAS gene. Homozygous seeds are collected and used to grow seedlings to be used in AHAS gene isolation.

DNA is extracted from 7 days old etiolated seedlings of a homozygous XI12 line. 60 g of plant tissue is powdered in liquid nitrogen, and transfered into 108 ml DNA extraction buffer (1.4 M NaCl, 2.0% Ctab (hexadecyl trimethyl ammonium bromide), 100 mM tris-Cl pH 8.0, 20 mM EDTA, 2% Mercaptoethanol) and 54 ml water. After incubation at 50-60°C for 30 minutes the suspension is extracted with an equal amount of chloroform. The DNA is precipitated by adding an equal amount of precipitation buffer (1% Ctab, 50 mM Tris-Cl pH 8.0, 10 mM EDTA). To purify the genomic DNA, a high speed centrifugation in 6.6M CsCl and ethidium bromide is performed (Ti80 rotor, 50,000 rpm, 20°C, 24 hours). The purified DNA is extracted with salt saturated Butanol and dialyzed for 25 hours against 3 changes of 1 I dialysis buffer (10 mM Tris-Cl Ph 8.0, 1 mM EDTA, 0.1M NaCl). The concentration of the XI12 genomic DNA is determined spectrophotometrically to be 310 mg/ml. The yield is 0.93 mg.

The XI12 genomic DNA is used to create a genomic library in the phage EMBL-3. The DNA is partially digested with Mbol and the fragments are separated on a sucrose gradient to produce size range between 8 to 22 kb before cloning into the BamHl site of EMBL-3. After obtaining 2.1 x 10⁶ independent clones, the library is amplified once. The titer of the library is determined 9 x 10¹⁰ pfu/ml.

To obtain probes for analysis of the XI12 library, a W22 (wild-type) cDNA library in lambda gt11, purchased from Clontech Inc., CA, is screened with an 800 nt BamH1 probe isolated from Arabidopsis AHAS genomic clone. The phages are plated in a density of 50,000 pfu/15 cm plate, transferred onto nitrocellulose filters, prehybridized in 6x SSC, 0.2% SDS for 2 hours and hybridized with the Arabidopsis AHAS probe in 6x SSC, 0.2% SDS overnight. One positive phage is identified, further purified and used for subcloning of a 1.1 kb EcoRI fragment. The 1.1 kb EcoRI fragment is subcloned into pGemA-4 and used as a probe to identify the XI12 AHAS genes.

The XI12 genomic library is plated on 12 15-cm plates (concentration of 50,000 pfu/plate) and is screened with the W22 AHAS cDNA probe. The filters are prehybridized (2 hours) and hybridized (over night) in Church buffer (0.5 M Na Phosphate, 1 mM EDTA, 1% BSA, 7% SDS) at 65°C and washed at 65°C in 2x SSC, 0.2% SDS and 0.3 x SSC, 0.2% SDS. 12 positive plaques are obtained from a total of 7.5 x 10⁵ pfu screened and 5 positive clones are further purified and isolated according to Chisholm (BioTechniques 7:21-23, 1989). Southern analysis (See Figure 2) showed that the phage clones represented two types of ĀHAS clones: Type-1 clones contain one large Xbal (>6.5 kb) fragment hybridizing to the AHAS cDNA probe, Type-2 clones contained two 2.7 and 3.7 kb Xbal fragments hybridizing to the AHAS cDNA probe. Genomic Southern of XI12 DNA demonstrated, that the Xbal fragments obtained by digesting genomic DNA and by hybridizing to the AHAS cDNA probe correspond to the Xbal fragments identified in the XI12 phage clones (See Figure 3). Restriction digest and Southern Analysis also demonstrate that of the 5 AHAS clones, one clone represents the mutant als2 genes and four represent the als1 gene.

The AHAS genes corresponding to the mutant locus located on chromosome 5 (clone 12/8A) and the non-mutant locus located on chromosome 4 (clone 12/17A) are subcloned as a Pstl fragment (clone 12/8A) or as Xbal fragment (12/17A) into the sequencing vector pBluescript II KSm13(+) (pKS+; Stratagene). Both 2.7 kb and 3.7 kb Xbal fragments from phage 12/17A contain one complete copy of AHAS genes which are identified. The sequence of each is obtained by dideoxy sequencing (Pharmacia T7 sequencing Kits) using primers complementary to the AHAS coding sequence.

The methods of DNA extraction, cloning of the genomic library and screening of the library are as described for the XI12 genomic DNA. The B73 AHAS genes are subcloned into the sequencing vector pKS+ as Xbal fragments and are sequenced. The sequence is obtained by dideoxy sequencing, using primers complementary to the AHAS coding sequence as described for the SI12 AHAS genes.

A W22 genomic library in EMBL3 purchased from Clontech Inc., CA is screened. The phages are plated in a density of 50,000 pfu/7 inch plate, transferred onto nitrocellulose filters, and hybridized with the W22 AHAS cDNA probe described above (prehybridization and hybridization conditions: 6 x SSC, 0.5% SDS, 1X Denhard's 100 mg/ml calf thymus DNA, 65°C, washing conditions: 3X x SSC, 0.2% SDS for 2 hours at 65°C, and 0.3 x SSC, 0.2% SDS for 2 hours). Two positive phages (12/1A and 12/4-4) are identified and further purified.

The W22 genomic clone 12/1A is subcloned as two 0.78 kb (pGemA-4) and 3.0 kb (pGemA-14; Promega) Sall fragments into the vector pGem-A2, and as a 6.5 kb Xbal fragment into the vector pKS+ (pCD200). The coding strand sequence of the W22 AHAS gene is obtained by dideoxy sequencing of

nested deletions created from subclones pGem A-14 and pGem A-4 of phage 12-1A. This sequence is used to design oligonucleotides complementary to the AHAS non-coding strand. The sequence of the non-coding strand is obtained by dideoxy sequencing of clone pCD200 using primers complementary to the coding strand. Upon complementing the sequencing of the W22 AHAS gene, primers of both DNA strands are designed and used for the sequencing of the AHAS genes isolated from the XI12 and B73 genomic libraries.

4. Cloning of QJ22 AHAS Genes

The sequence of the gene encoding AHAS in the maize line QJ22, which is selectively resistant to imidazolinones, is also determined. A genomic library of QJ22 is prepared in an EMBL3 vector. A library of 800,000 phage is screened with an 850 nucleotide Sall/Clal fragment isolated from an AHAS clone (A-4) derived from the wild-type maize line W22. Five positive phages are picked and submitted to a second round of screening to partially purify the phage. The partially purified phage are analyzed by PCR to determine if any clones represent the QJ22 alsl gene. Such clones are identified as a 3.7kb Xbal fragment with a gene specific Smal site at position 495. The second screen indicates the presence of a single positive clone with these characteristics.

The PCR product is purified using a commercial kit (Magic PCR Preps) from Promega, and the purified DNA is sequenced with a Taq polymerase sequencing system "fmol", also from Promega Sequence analysis of both strands of the DNA of the QJ22 mutant AHAS shows a nucleotide transition from G to A in the codon for amino acid 621. This mutation is identical to the one seen in XI12 and the remainder of the sequence is typical of an als1 gene.

RESULTS

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The sequence of the mutant AHAS genes is compared with the sequences obtained from the wild type corn lines B73 and W22 (See Figure 7). The XI12 mutant gene (XI12/8A) and the QJ22 mutant gene and the wild type gene are identical except for the amino acid change at position 621, causing a single nucleotide transition from AGT to AAT (See Figure 8). The XI12 mutant XI12/8A and the wild-type B73/7-4 gene show an additional difference at position 63. On the other hand, the non-mutant XI12 AHAS gene cloned in XI12/17A is completely homologous to the corresponding B73/10-2 in the region coding for the mature AHAS protein (data not shown).

DEPOSIT OF BIOLOGICAL MATERIALS

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The following biological materials were deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland, 20857, as follows:

E. coli XLI Blue harboring plasmid pX12/8A, deposited on July 3, 1991, Accession Number ATCC 68643

XI12 corn seed deposited on July 16, 1991, Accession Number ATCC 75051.

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Sequence Listings

| 5 | Segi | lenc | e ID | No. | : 1 | | | | | | | | |
|----|------|--------|-------|-------|-------------|-------|-------------|---------------|-------|------|------|------|-----|
| | Seqı | lenc | э туј | e: | Nuc: | leot: | ide : | and 2 | Amin | o Ac | id | | |
| 10 | Seqı | leuc (| e Lei | ngth: | : 1! | 969 I | BP's | and | 638 | Ami | no A | cids | |
| 15 | Stra | ande | dnes | 3: £ | Sing: | le | | | | | | | |
| | Topo | ology | y: 1 | Linea | 2. r | | | | | | | | |
| 20 | Ori | ginal | l Soi | ırce | Orga | anisı | n: <u>1</u> | 7 <u>08</u> 1 | nays | | | | |
| | Prop | perti | ies: | Hei | rbic: | ide 1 | Resi | stani | t and | as e | usAu | 2 | |
| 25 | | | | | | | | | | | | | |
| | AACO | CCTC | SCG (| cccc | CTCC | ga gi | ACAG | CCGC | C GC | AACC | | | 36 |
| 30 | ATG | GCC | ACC | GCC | GCC | GCC | GCG | TCT | ACC | GCG | CTC | act | 72 |
| | Met | Ala | Thr | Ala | Ala | Ala | Ala | Ser | Thr | Ala | Leu | Thr | |
| | 1 | | | | 5 | | | | | 10 | | | |
| 35 | | | | | | | | | | | | | |
| | GGC | GCC | ACT | ACC | GCT | GCG | CCC | AAG | GCG | AGG | CGC | CGG | 108 |
| | Gly | Ala | Thr | Thr | Ala | Ala | Pro | ГÄЗ | Ala | Arg | Arg | Arg | |
| 40 | | | 15 | | | | | 20 | | | | | |
| | | | | | | | | | | | | | |
| | GCG | CAC | CTC | CTG | GCC | ACC | CGC | CGC | GCC | CTC | GCC | GCG | 144 |
| | Ala | His | Leu | Leu | Ala | Thr | Arg | Arg | Ala | Leu | Ala | Ala | |
| 45 | 25 | | | | | 30 | | | | | 35 | | |
| | | | | | | | | | | | | | |
| | | | | TGC | | | | | | | | | 180 |
| 50 | Pro | Ile | Arg | Cys | Ser | Ala | Ala | Ser | Pro | Ala | Met | Pro | |
| | | | | 40 | | | | | 45 | | | | |

| 5 | ATG | GCT | CCC | CCG | GCC | ACC | CCG | CTC | CGG | CCG | TGG | GGC | 216 |
|----|-------------|-------|------|------|-----|-----|-----|-----|----------|-----|-----|------|-------|
| | Met | Ala | Pro | Pro | Ala | Thr | Pro | Leu | Arg | Pro | Trp | Gly | |
| | | 50 | | | | | 55 | | | | | 60 | |
| 10 | | | | | | | | | | | | | |
| 10 | ccc | ACC | GAT | ccc | CGC | AAG | GGC | GCC | GAC | ATC | CTC | GTC | 252 |
| | Pro | Thr | Asp | Pro | Arg | Lys | Gly | Ala | Asp | Ile | Leu | Val | |
| | | | | | 65 | | | | | 70 | | | |
| 15 | | | | | | | | | | | | | |
| | GAG | TCC | CTC | GAG | CGC | TGC | GGC | GTC | CGC | GAC | GTC | TTC | 288 |
| | Glu | Ser | Leu | Glu | Arg | Cys | Gly | Val | Arg | Asp | Val | Phe | |
| 20 | | | 75 | | | | | 80 | | | | | |
| | | | | | | | | | | | | | |
| | | | | | GGC | | | | | | | | 324 |
| 25 | | Tyr | Pro | Gly | Gly | Ala | Ser | Met | Glu | Ile | | Gln | |
| 20 | 85 | | | | | 90 | | | | | 95 | | |
| | | | | | | | | | | | | | |
| | | | | | TCC | | | | | | | | 360 |
| 30 | Ala | Leu | Thr | _ | Ser | Pro | Val | Ile | | Asn | His | Leu | |
| | | | | 100 | | | | | 105 | | | | |
| | | 000 | 03.0 | a. a | ~~~ | 000 | a.a | 222 | | 600 | 200 | maa. | 206 |
| 35 | | | | | CAA | | | | | | | | 396 |
| | Pne | _ | nis | GIU | Gln | GIY | 115 | AIG | Pne | Ald | ATG | 120 | |
| | | 110 | | | | | 113 | | | | | 120 | |
| 40 | GGC | TO C | ece | CGC | TCC | ሞርሬ | GGC | CGC | GT/C | GGC | GTC | ጥሮር | 432 |
| | | | | | ser | | | | | | | | 172 |
| | Gry | TYL | AIG | ALG | 125 | Del | GIJ | nry | V W.Z. | 130 | 741 | CIS | |
| | | | | | 123 | | | | | 130 | | • | |
| 45 | እጥ ር | GCC | ACC | TCC | GGC | CCC | GGC | GCC | ACC | AAC | СТТ | GTC | 468 |
| | | | | | Gly | | | | | | | | |
| | 110 | | 135 | 501 | 011 | | 1 | 140 | | | | | |
| 50 | | | | | | | | | | | | | |
| | TCC | GCG | СТС | GCC | GAC | GCG | CTG | CTC | GAT | TCC | GTC | ccc | 504 |
| | | | | | Asp | | | | | | | | - • • |
| 55 | 145 | ***** | | | | 150 | | | P | | 155 | | |
| | | | | | | | | | | | | | |

| 5 | ATG | GTC | GCC | ATC | ACG | GGA | CAG | GTG | CCG | CGA | CGC | ATG | 540 |
|----|-----|------------|-----|-----|-----|-----|-----|------------|-----|------------|-----|-----|-----|
| · | Met | Val | Ala | Ile | Thr | Gly | Gln | Val | Pro | Arg | Arg | Met | |
| | | | | 160 | | | | | 165 | | | | |
| | | | | | | | | | | | | | |
| 10 | ATT | GGC | ACC | GAC | GCC | TTC | CAG | GAG | ACG | ccc | ATC | GTC | 576 |
| | Ile | Gly | Thr | Asp | Ala | Phe | Gln | Glu | Thr | Pro | Ile | AST | |
| | | 170 | | | | | 175 | | | | | 180 | |
| 15 | | | | | | | | | | | | | • |
| | GAG | GTC | ACC | CGC | TCC | ATC | ACC | AAG | CAC | AAC | TAC | CTG | 612 |
| | Glu | Val | Thr | Arg | Ser | Ile | Thr | Lys | Ris | Asa | Tyr | Leu | |
| 20 | | | | | 185 | | | | | 190 | | | |
| | | | | | | | | | | | | | |
| | GTC | CTC | GAC | GTC | GAC | GAC | ATC | ccc | CGC | GTC | GTG | CAG | 648 |
| | Val | Leu | Asp | Val | Ąsp | Asp | Ile | Pro | Arg | Val | val | Gln | |
| 25 | | | 195 | | | | | 200 | | | | | |
| | | | | | | | | | | | | | |
| | GAG | GCT | TTC | TTC | CTC | GCC | TCC | TCT | GGT | CGA | CCG | GGG | 684 |
| 30 | Glu | Ala | Phe | Phe | Leu | Ala | ser | ser | Gly | Arg | Pro | Gly | |
| | 205 | | | | | 210 | | | | | 215 | | |
| | | | | | | | | | | | | | |
| 35 | CCG | GTG | CTT | GTC | GAC | ATC | CCC | AAG | GAC | ATC | CAG | CAG | 720 |
| | Pro | Val | Leu | Val | Asp | Ile | Pro | Lys | Asp | Ile | Gln | Gln | |
| | | | | 220 | | | | | 225 | | | | |
| 40 | | | | | | | | | | | | | |
| 40 | | | GCG | | | | | | | | | | 756 |
| | Gln | Met | Ala | Val | Pro | val | Trp | Asp | Lys | Pro | Met | | |
| | | 230 | | | | | 235 | | | | | 240 | |
| 45 | | | | | | | | | | | | | |
| | | | | | | | | | | | | CCT | 792 |
| | Leu | Pro | Gly | Tyr | Ile | Ala | Arg | Leu | Pro | | Pro | Pro | |
| 50 | | | | | 245 | | | | | 250 | | | |
| | | | | | | | | | | | | | |
| | | | GAG | | | | | | | | | | 828 |
| | Ala | Thr | Glu | Leu | Leu | Glu | Gln | | Leu | Arg | Leu | Val | |
| 55 | | | 255 | | | | | 260 | | | | | |

| | GGT | GAA | TCC | CGG | CGC | CCT | GTT | CTT | TAT | GTT | GGC | GGT | 864 |
|----|------------|-----|-----|-----|------------|-----|------------|------------|-----|----------------|-----|------------|------|
| 5 | Gly | Glu | Ser | Arg | Arg | Pro | val | Leu | Tyr | Avj | Gly | Gly | |
| | 265 | | | | | 270 | | | | | 275 | | |
| | | | | | | | | | | | | | |
| 10 | GCG | TGC | GCA | GCA | TCT | GGT | GAG | GAG | TTG | CGA | CGC | TTT | 900 |
| 10 | Ala | Cys | Ala | Ala | ser | Gly | Glu | Glu | Leu | Arg | Arg | Phe | |
| | | | | 280 | | | | | 285 | | | | |
| | | | | | | | | | | | | | |
| 15 | GTG | GAG | CTG | act | GGA | ATC | CCG | GTC | ACA | act | act | CTT | 936 |
| | Val | Glu | Leu | Thr | Gly | Ile | Pro | Val | Thr | Thr | Thr | Leu | |
| | | 290 | | | | | 295 | | | | | 300 | |
| 20 | | | | | | | | | | | | | |
| | atg | GGC | CTC | GGC | AAC | TTC | ccc | AGC | GAC | GAC | CCA | CTG | 972 |
| | Met | Gly | Leu | Gly | Asn | Phe | Pro | ser | Asp | Asp | Pro | Leu | |
| 25 | | | | | 305 | | | | | 310 | | | |
| 25 | | | | | | | | | | | | | |
| | TCT | CTG | CGC | ATG | CTA | GGT | ATG | CAT | GGC | ACG | GTG | TAT | 1008 |
| | Ser | Leu | Arg | Met | Leu | Gly | Met | His | Gly | Thr | Asj | Tyr | |
| 30 | | | 315 | | | | | 320 | | | | | |
| | | | | | | | | | | | | | |
| | GCA | aat | TAT | GCA | GTG | GAT | AAG | GCC | Gat | CTG | TTG | CTT | 1044 |
| 35 | Ala | Asn | Tyr | Ala | val | Asp | ГÄЗ | Ala | ysb | Leu | Leu | Leu | |
| | 325 | | | | | 330 | | | | | 335 | | |
| | | | | | | | | | | | | | |
| 40 | GCA | CTT | GGT | GTG | CGG | TTT | GAT | GAT | CGT | GTG | ACA | GGG | 1080 |
| 40 | Ala | Leu | GJÅ | Avj | Arg | Phe | Asp | Asp | Arg | V&1 | Thr | Gly | |
| | | | | 340 | | | | | 345 | | | | |
| | | | | | | | | | | | | | |
| 45 | AAG | ATT | GAG | GCT | TTT | GCA | AGC | AGG | GCT | AAG | ATT | GTG | 1116 |
| | ГÄЗ | Ile | Glu | Ala | Phe | Ala | Ser | Arg | Ala | Lys | Ile | Val | |
| | | 350 | | | | | 355 | | | | | 360 | |
| 50 | | | | | | | | | | | | | |
| | CAC | GTT | GAT | ATT | gat | CCG | GCT | GAG | ATT | GGC | AAG | AAC | 1152 |
| | His | Val | Asp | Ile | Asp | Pro | Ala | Glu | Ile | Gly | Lys | Asn | |
| EE | | | | | 365 | | | | | 370 | | | |
| 55 | | | | | | | | | | | | | |

| | AAG | CAG | CCA | CAT | GTG | TCC | ATC | TGT | GCA | GAT | GTT | AAG | 1188 |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | Lys | Gln | Pro | His | Val | Ser | Ile | Cys | Ala | Asp | Val | Lys | |
| 5 | | | 375 | | | | | 380 | | | | | |
| | | | | | | | | | | | | | |
| | CTT | GCT | TTG | CAG | GGC | ATG | AAT | GCT | CTT | CTT | GAA | GGA | 1224 |
| | Leu | Ala | Leu | Gln | Gly | Met | Asn | Ala | Leu | Leu | Glu | Gly | |
| 10 | 385 | | | | | 390 | | | | | 395 | | |
| | | | | | | | | | | | | | |
| | AGC | ACA | TCA | AAG | AAG | AGC | TTT | GAC | TTT | GGC | TCA | TGG | 1260 |
| 15 | Ser | Thr | Ser | Lys | Lys | Ser | Phe | Asp | Phe | Gly | Ser | Trp | |
| | | | | 400 | | | | | 405 | | | | • |
| | | | | | | | | | | | | | |
| 20 | AAC | GAT | GAG | TTG | GAT | CAG | CAG | AAG | AGG | GAA | TTC | ccc | 1296 |
| | Asn | Asp | Glu | Leu | Asp | Gln | Gln | Lys | Arg | Glu | Phe | Pro | |
| | | 410 | | | | | 415 | | | | | 420 | |
| | | | | | | | | | | | | | |
| 25 | CTT | GGG | TAT | AAA | ACA | TCT | AAT | GAG | GAG | ATC | CAG | CCA | 1332 |
| | Leu | Gly | Tyr | Lys | Thr | Ser | Asn | Glu | Glu | Ile | Gln | Pro | |
| | | | | | 425 | | | | | 430 | | | |
| 30 | | | | | | | | | | | | | |
| | CAA | TAT | GCT | ATT | CAG | GTT | CTT | GAT | GAG | CTG | ACG | AAA | 1368 |
| | Gln | Tyr | Ala | Ile | Gln | Val | Leu | Asp | Glu | Leu | Thr | Lys | |
| 35 | | | 435 | | | | | 440 | | | | | |
| | | | | | | | | | | | | | |
| | | | | ATC | | | | | | | | | 1404 |
| | Gly | Glu | Ala | Ile | Ile | Gly | Thr | Gly | Val | Gly | | His | |
| 40 | 445 | | | | | 450 | | | | | 455 | | |
| | | | | | | | | | | | | | |
| | | | | | | | | | | | | CGG | 1440 |
| 45 | Gln | Met | Trp | Ala | Ala | Gln | Tyr | Tyr | Thr | Tyr | ГÄЗ | Arg | |
| | | | | 460 | | | | | 465 | | | | |
| | | | | | | | | | | | | | |
| 50 | | | | TGG | | | | | | | | | 1476 |
| | Pro | Arg | Gln | Trp | Leu | Ser | Ser | Ala | Gly | Leu | Gly | | |
| | | 470 | | | | | 475 | | | | | 480 | |

| | ATG | GGA | TTT | GGT | TTG | CCG | GCT | GCT | GCT | GGT | GCT | TCT | 1512 |
|-----------|-------------|------|------|-----|------|------|-------------|------|------------|-----------------|--------|-----|------|
| | Met | Gly | Phe | Gly | Leu | Pro | Ala | Ala | Ala | Gly | Ala | Ser | |
| 5 | | | | | 485 | | | | | 490 | | | |
| • | | | | | | | | | | | | | |
| | GTG | GCC | AAC | CCA | GGT | GTT | act | GTT | GTT | GAC | atc | gat | 1548 |
| | Val | Ala | Asn | Pro | Gly | val | Thr | Val | Val | Asp | Ile | Asp | |
| 10 | | | 495 | | | | | 500 | | | | | |
| | | | | | | | | | | | | | |
| | GGA | gat | GGT | AGC | TTT | CTC | ATG | AAC | GTT | CAG | GAG | CTA | 1584 |
| 15 | Gly | Asp | Gly | Ser | Phe | Leu | Met | Asn | val | Gln | Glu | Leu | |
| | 505 | | | | | 510 | | | | | 515 | | |
| | | | | | | | | | | | | | |
| 20 | | | | | | | | | | | | GTC | 1620 |
| | Ala | Met | Ile | _ | Ile | Glu | ASD | Leu | | AST | гÄз | AST | |
| | | | | 520 | | | | | 525 | | | | |
| 25 | eth E01 E71 | ce c | OM D | 224 | 224 | ~~ ~ | ~ | OM C | ccc | _ከ መሮ | CMC. | GTG | 1656 |
| | | | | | Asn | | | | | | | | 7020 |
| | Pus | 530 | neu | asu | ASII | GTII | 535 | пеп | OTA | Mec | V 62.2 | 540 | |
| | | 530 | | | | | J JJ | | | | | 346 | |
| 30 | CAG | TGG | GAG | GAC | »GG | TTC | TAT | AAG | GCC | AAC | AGA | GCG | 1692 |
| | | | | | Arg | | | | | | | | |
| | | | | & | 545 | | 2 | • | | 550 | - | | |
| 35 | | | | | | | | | | | | | |
| | CAC | ACA | TAC | TTG | GGA | AAC | CCA | GAG | AAT | GAA | agt | GAG | 1728 |
| | His | Thr | Tyr | Leu | Gly | Asn | Pro | Glu | Asn | Glu | ser | Glu | |
| 40 | | | 555 | | | | | 560 | | | | | |
| | | | | | | | | | | | | | |
| | ATA | TAT | CCA | GAT | TTC | GTG | ACG | ATC | GCC | AAA | GGG | TTC | 1764 |
| 45 | Ile | Tyr | Pro | Asp | Phe | Val | Thr | Ile | Ala | Lys | Gly | Phe | |
| | 565 | | | | | 570 | | | | | 575 | | |
| | | | | | | | | | | | | | |
| 50 | | | | | | | | | | | | GAA | 1800 |
| 50 | Asn | Ile | Pro | Ala | Val | Arg | Val | Thr | | Lys | Asn | Glu | |
| | | | | 580 | | | | | 585 | | | | |

| | GTC | CGC | GCA | GCG | ATA | AAG | AAG | ATG | CTC | GAG | act | CCA | 1836 |
|----|------------|------|------------|-------|--------------|-----|-----|-----|-------------|-----|-----|------------|------|
| | Val | Arg | Ala | Ala | Ile | Lys | Lys | Met | Leu | Glu | Thr | Pro | |
| 5 | | 590 | | | | | 595 | | | | | 600 | |
| | | | | | | | | | | | | | |
| | GGG | CCG | TAC | CTC | TTG | gat | ata | atc | GTC | CCA | CAC | CAG | 1872 |
| 10 | Gly | Pro | Tyr | Leu | Leu | Asp | Ile | Ile | Val | Pro | His | Gla | |
| 10 | | | | | 605 | | | | | 610 | | | |
| | | | | | | | | | | | | | |
| | GAG | CAT | GTG | TTG | CCT | atg | ATC | CCT | r aa | GGT | GGG | GCT | 1908 |
| 15 | Glu | His | Val | Leu | Pro | Met | Ile | Pro | Asn | Gly | Gly | Ala | |
| | | | 615 | | | | | 620 | | | | | |
| | | | | | | | | | | | | | |
| 20 | TTC | AAG | GAT | ATG | ATC | CTG | Gat | GGT | gat | GGC | AGG | act | 1944 |
| | Phe | Lys | Asp | Met | Ile | Leu | Asp | Gly | Asp | Gly | Arg | Thr | |
| | 625 | | | | | 630 | | | | | 635 | | |
| | | | | | | | | | | | | | |
| 25 | GTG | TAC | | | | | | | | | | | 1950 |
| | Val | Tyr | | | | | | | | | | | |
| | | 638 | | | | | | | | | | | |
| 30 | | | | | | | | | | | | | |
| | TGA: | CTAI | AAA! | rcca(| CAA (| 3 | | | | | | | 1969 |
| | | | | | | | | | | | | | |
| | | | | | | | | | | | | | |

| | sequence ID No.: 2 | |
|----|---|-----|
| 5 | Sequence Type: Nucleotide and Amino Acid | |
| 10 | Sequence Length: 1969 BP's and 638 Amino Acids | |
| ,, | Strandedness: Single | |
| 15 | Topology: Linear | |
| | Original Source Organism: Zea mays | |
| 20 | Properties: Herbicide Sensitive AHAS Enzyme | |
| | | |
| 25 | AACCCTCGCG CCGCCTCCGA GACAGCCGCC GCAACC | 36 |
| | ATG GCC ACC GCC GCC GCG TCT ACC GCG CTC ACT | 72 |
| 30 | Met Ala Thr Ala Ala Ala Ser Thr Ala Leu Thr | |
| | 1 5 10 | |
| | . GGC GCC ACT ACC GCT GCG CCC AAG GCG AGG CGC CGG | 108 |
| 35 | Gly Ala Thr Thr Ala Ala Pro Lys Ala Arg Arg Arg | 100 |
| | 15 20 | |
| | | |
| 40 | GCG CAC CTC CTG GCC ACC CGC CGC GCC CTC GCC GCG | 144 |
| | Ala His Leu Leu Ala Thr Arg Arg Ala Leu Ala Ala | |
| | 25 30 35 | |
| 45 | | |
| | CCC ATC AGG TGC TCA GCG GCG TCA CCC GCC ATG CCG | 180 |
| | Pro Ile Arg Cys Ser Ala Ala Ser Pro Ala Met Pro 40 45 | |
| 50 | 7.7 T.7 | |
| | ATG GCT CCC CCG GCC ACC CCG CTC CGG CCG TGG GGC | 216 |
| | Met Ala Pro Pro Ala Thr Pro Leu Arg Pro Trp Gly | |
| 55 | 50 55 60 | |

| | CCC | ACC | GAT | CCC | CGC | AAG | GGC | GCC | GAC | ATC | CTC | GTC | 252 |
|----|-----|-----|-----|-----|-----|-----|------------|-----|------------|-----|-----|-----|-------------|
| 5 | Pro | Thr | Asp | Pro | Arg | Lys | Gly | Ala | Asp | Ile | Leu | ASJ | |
| | | | | | 65 | | | | | 70 | | | |
| | | | | | | | | | | | | | |
| 10 | GAG | TCC | CTC | GAG | CGC | TGC | GGC | GTC | CGC | GAC | GTC | TTC | 288 |
| 70 | Glu | Ser | Leu | Glu | Arg | Cys | Gly | Val | Arg | Asp | Val | Phe | |
| | | | 75 | | | | | 80 | | | | | |
| | | | | | | | | | | | | | |
| 15 | GCC | TAC | ccc | GGC | GGC | GCG | TCC | atg | GAG | atc | CAC | CAG | 324 |
| | Ala | Tyr | Pro | Gly | Gly | Ala | Ser | Met | Glu | Ile | Nis | Gln | |
| | 85 | | | | | 90 | | | | • | 95 | | |
| 20 | | | | | | | | | | | | | |
| | GCA | CTC | ACC | CGC | TCC | ccc | GTC | ATC | GCC | AAC | CAC | CTC | 360 |
| | Ala | Leu | Thr | Arg | Ser | Pro | Val | Ile | Ala | Asn | His | Leu | |
| 25 | | | | 100 | | | | | 105 | | | | |
| 25 | | | | | | | | | | | | | |
| | TTC | CGC | CAC | GAG | CAA | GGG | GAG | GCC | TTT | GCG | GCC | TCC | 396 |
| | Phe | Arg | His | Glu | Gln | Gly | Glu | Ala | Phe | Ala | Ala | Ser | |
| 30 | | 110 | | | | | 115 | | | | | 120 | |
| | | - | | | | | | | | | | | |
| | GGC | TAC | GCG | CGC | TCC | TCG | GGC | CGC | GTC | GGC | GTC | TGC | 432 |
| 35 | Gly | Tyr | Ala | Arg | Ser | Ser | Gly | Arg | Val | Gly | Avj | Суз | |
| | | | | | 125 | | | | | 130 | | | |
| | | | | | | | | | | | | | |
| 40 | | | | TCC | | | | | | | | | 468 |
| | Ile | Ala | Thr | Ser | Gly | Pro | Gly | Ala | Thr | Asn | Leu | A9J | |
| | | | 135 | | | | | 140 | | | | | |
| | | | | | | | | | | | | | |
| 45 | | | | GCC | | | | | | | | | 50 4 |
| | Ser | Ala | Leu | Ala | Asp | Ala | Leu | Leu | Asp | Ser | Val | Pro | |
| | 145 | | | | | 150 | | | | | 155 | | |
| 50 | | | | | | | | | | | | | |
| | | | | ATC | | | | | | | | | 540 |
| | Met | Val | Ala | Ile | Thr | Gly | Gln | Val | Pro | Arg | Arg | Met | |
| 55 | | | | 160 | | | | | 165 | | | | |
| | | | | | | | | | | | | | |

| 5 | ATT | GGC | ACC | GAC | GCC | TTC | CAG | GAG | ACG | CCC | ATC | GTC | 576 |
|-----|-----|------------|-----|------------|-----|-----|-----|------------|-----|-----|-----|------------|-----|
| | Ile | Gly | Thr | Asp | Ala | Phe | Gln | Glu | Thr | Pro | Ile | Val | |
| | | 170 | | | | | 175 | | | | | 180 | |
| | | | | | | | | | | | | | |
| 10 | GAG | GTC | ACC | CGC | TCC | ATC | ACC | AAG | CAC | AAC | TAC | CTG | 612 |
| | Glu | Val | Thr | Arg | Ser | Ile | Thr | Lys | His | Asn | Tyr | Leu | |
| | | | | | 185 | | | | | 190 | | | |
| 15 | | | | | | | | | | | | | |
| | GTC | CTC | GAC | GTC | GAC | GAC | ATC | CCC | CGC | GTC | GTG | CAG | 648 |
| | Val | Leu | Asp | val | Asp | Asp | Ile | Pro | Arg | Wal | Wal | Gln | |
| 20 | | | 195 | | | | | 200 | | | | | |
| | | | | | | | | | | | | | |
| | GAG | GCT | TTC | TTC | CTC | GCC | TCC | TCT | GGT | CGA | CCG | GGG | 684 |
| | Glu | Ala | Phe | Phe | Leu | Ala | Ser | Ser | Gly | Arg | Pro | Gly | |
| 25 | 205 | | | | | 210 | | | | | 215 | | |
| | | | | | • | | | | | | | | |
| | CCG | GTG | CTT | GTC | GAC | ATC | ccc | AAG | GAC | ATC | CAG | CAG | 720 |
| 30 | Pro | val | Leu | Avj | Asp | Ile | Pro | Lys | Asp | Ile | Gln | Gln | |
| | | | | 220 | | | | | 225 | | | | |
| | | | | | | | | | | | | | |
| 35 | CAG | ATG | GCG | GTG | CCT | GTC | TGG | GAC | AAG | CCC | atg | agt | 756 |
| | Gln | Met | Ala | Val | Pro | Val | Trp | Asp | Lys | Pro | Met | ser | |
| | | 230 | | | | | 235 | | | | | 240 | |
| | | | | | | | | | | | | | |
| 40 | CTG | CCT | GGG | TAC | ATT | GCG | CGC | CTT | CCC | AAG | CCC | CCT | 792 |
| | Leu | Pro | Gly | Tyr | Ile | Ala | Arg | Leu | Pro | Lys | Pro | Pro | |
| | | | | | 245 | | | | | 250 | | | |
| 45 | | | | | | | | | | | | | |
| | GCG | ACT | GAG | TTG | CTT | GAG | CAG | GTG | CTG | CGT | CTT | GTT | 828 |
| | Ala | Thr | Glu | Leu | Leu | Glu | Gln | Val | Leu | Arg | Leu | Val | |
| 50 | | | 255 | | | | | 260 | | | | | |
| · · | | | | | | | | | | | | | |
| | GGT | GAA | TCC | CGG | CGC | CCT | GTT | CTT | TAT | GTT | GGC | GGT | 864 |
| | Gly | Glu | Ser | Arg | Arg | Pro | Wal | Leu | Tyr | Val | Gly | Gly | |
| 55 | 265 | | | | | 270 | | | | | 275 | | |

| | GCG | TGC | GCA | GCA | TCT | GGT | GAG | GAG | TTG | CGA | CGC | TTT | 900 |
|----|------------|-----|-----|-----|-----|-----|-----|---------|-----|-------------|-----|-----|------|
| 5 | Ala | Cys | Ala | Ala | Ser | Gly | Glu | Glu | Leu | Arg | Arg | Phe | |
| | | | | 280 | | | | | 285 | | | | |
| | | | | | | | | | | | | | |
| 10 | GTG | GAG | CTG | ACT | GGA | ATC | CCG | GTC | ACA | ACT | ACT | CTT | 936 |
| | Val | Glu | Leu | Thr | Gly | Ile | Pro | Val | Thr | Thr | Thr | Leu | |
| | | 290 | | | | | 295 | | | | | 300 | |
| 15 | | | | | | | | | | | | | |
| | ATG | GGC | CTC | GGC | AAC | TTC | ccc | AGC | GAC | GAC | CCA | CTG | 972 |
| | Met | Gly | Leu | Gly | Asn | Phe | Pro | ser | yab | Asp | Pro | Leu | • |
| | | | | | 305 | | | | | 310 | | | |
| 20 | | | | | | | | | | | | | |
| | TCT | CTG | CGC | ATG | CTA | GGT | ATG | CAT | GGC | ACG | GTG | TAT | 1008 |
| | Ser | Leu | Arg | Met | Leu | Gly | Met | His | Gly | Thr | Val | Tyr | |
| 25 | | | 315 | | | | | 320 | | | | | |
| | | | | | | | | | | | | | |
| | | | | | | | | | | | | CTT | 1044 |
| 30 | Ala | Asn | Tyr | Ala | Val | Asp | Lys | Ala | Asp | Leu | | Leu | • |
| | 325 | | | | | 330 | | | | | 335 | | |
| | | | | | | | | | | | | | |
| | | | | | | | | | | | | GGG | 1080 |
| 35 | Ala | Leu | Gly | | Arg | Phe | Asp | yab | | Val | Thr | Gly | |
| | | | | 340 | | | | | 345 | | | | |
| | | | | | | | | | | | | | |
| 40 | | | | | | | | | | | | GTG | 1116 |
| | Lys | | Glu | Ala | Phe | Ala | | Arg | Ala | Lys | Ile | | |
| | | 350 | | | | | 355 | | | | | 360 | |
| 45 | | | | | | | | | | | | | 4450 |
| | | | | | | | | | | | | AAC | 1152 |
| | His | Val | Asp | Ile | _ | Pro | Ala | GIU | IIe | Gly | гля | ASD | |
| 50 | | | | | 365 | | | | | 370 | | | |
| 50 | | | | | | | | | | ~ *- | ar- | | 4400 |
| | | | | | | | | | | | | AAG | 1188 |
| • | Lys | Gln | | His | Val | ser | 116 | _ | Ala | Asp | VAI | гаа | |
| 55 | | | 375 | | | | | 380 | | | | | |

| | CTT | GCT | TTG | CAG | GGC | ATG | AAT | GCT | CTT | CTT | GAA | GGA | 1224 |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | Leu | Ala | Leu | Gln | Gly | Met | Asn | Ala | Leu | Leu | Glu | Gly | |
| 5 | 385 | | | | | 390 | | | | | 395 | | |
| | | | | | | | | | | | | | |
| | AGC | ACA | TCA | AAG | AAG | AGC | TTT | GAC | TTT | GGC | TCA | TGG | 1260 |
| | Ser | Thr | Ser | Lys | Lys | Ser | Phe | Asp | Phe | Gly | Ser | Trp | |
| 10 | | | | 400 | | | | | 405 | | | | |
| | | | | | | | | | | | | | |
| | AAC | GAT | GAG | TTG | GAT | CAG | CAG | AAG | AGG | GAA | TTC | CCC | 1296 |
| 15 | Asn | Asp | Glu | Leu | Asp | Gln | Gln | Lys | Arg | Glu | Phe | Pro | |
| | | 410 | | | | | 415 | | | | | 420 | |
| | | | | | | | | | | | | | |
| 20 | CTT | GGG | TAT | AAA | ACA | TCT | AAT | GAG | GAG | ATC | CAG | CCA | 1332 |
| | Leu | Gly | Tyr | Lys | Thr | Ser | Asn | Glu | Glu | Ile | Gln | Pro | |
| | | | | | 425 | | | | | 430 | | | |
| | | | | | | | | | | | | | |
| 25 | CAA | TAT | GCT | ATT | CAG | GTT | CTT | GAT | GAG | CTG | ACG | AAA | 1368 |
| | Gln | Tyr | Ala | Ile | Gln | Val | Leu | Asp | Glu | Leu | Thr | Lys | |
| | | | 435 | | | | | 440 | | | | | |
| 30 | | | | | | | | | | | | | |
| | | | | | | | | | | | | CAC | 1404 |
| | Gly | Glu | Ala | Ile | Ile | Gly | Thr | Gly | Val | Gly | Gln | His | |
| 35 | 445 | | | | | 450 | | | | | 455 | | |
| | | | | | | | | | | | | | |
| | | | TGG | | | | | | | | | | 1440 |
| | Gln | Met | Trp | Ala | Ala | Gln | Tyr | Tyr | Thr | Tyr | Lys | Arg | |
| 40 | | | | 460 | | | | | 465 | | | | |
| | | | | | | | | | | | | | |
| | | | CAG | | | | | | | | | | 1476 |
| 45 | Pro | Arg | Gln | Trp | Leu | Ser | Ser | Ala | Gly | Leu | Gly | Ala | |
| | | 470 | | | | | 475 | | | | | 480 | |
| | | | | | | | | | | | | | |
| 50 | ATG | GGA | TTT | GGT | TTG | CCG | GCT | GCT | GCT | GGT | GCT | TCT | 1512 |
| | Met | Gly | Phe | Gly | Leu | Pro | Ala | Ala | Ala | Gly | Ala | Ser | |
| | | | | | 485 | | | | | 490 | | | |

| | 650 | 000 | 000 | ~~~ | ~~~ | 000 | 5 AB | ann. | ~~~ | <i>ana</i> | 2000 | 4 0.69 | 9 5 4 6 |
|----|-------|-----|-----|--------------------|------|------|-------------|------|-------------|------------|------------|---------------|---------|
| | | | | | | | | | | | | GAT - | 1548 |
| | V&1 | Ala | Asn | Pro | Gly | Va1 | Thr | Val | Agi | Asp | Ile | Asp | |
| 5 | | | 495 | | | | | 500 | | | | | |
| | | | | | | | | | | | | | |
| | GGA | GAT | GGT | AGC | TTT | CTC | atg | AAC | gtt | CAG | GAG | CTA | 1584 |
| | Gly | Asp | Gly | ser | Phe | Leu | Met | asa | Asj | Gln | Glu | Leu | |
| 10 | 505 | | | | | 510 | | | | | 515 | | |
| | | | | | | | | | | | | | |
| | GCT | atg | ATC | CGA | ATT | GAG | AAC | CTC | CCG | GTG | AAG | GTC | 1620 |
| 15 | Ala | Met | Ile | Arg | Ile | Glu | Asn | Leu | Pro | Wal | Lys | Val | • |
| | | | | 520 | | | | | 525 | | | | |
| | | | | | | | | | | | | | |
| | TTT | GTG | CTA | AAC | AAC | CAG | CAC | CTG | GGG | ATG | GTG | GTG | 1656 |
| 20 | Phe | Val | Leu | Asn | Asn | Gln | His | Leu | Gly | Met | Val | v al | |
| | | 530 | | | | | 535 | | | | | 540 | |
| | | | | | | | | | | | | | |
| 25 | CAG | TGG | GAG | GAC | AGG | TTC | TAT | AAG | GCC | AAC | AGA | GCG | 1692 |
| | Gln | Trp | Glu | Asp | Arg | Phe | Tyr | Lys | Ala | Asn | Arg | Ala | |
| | | _ | | • | 545 | | - | - | | 550 | _ | | |
| 30 | | | | | | | | | | | | | |
| 00 | CAC | ACA | TAC | TTG | GGA | AAC | CCA | GAG | aan Taak | GAA | agt | GAG | 1728 |
| | | | Tyr | | | | | | | | | | |
| | | | 555 | | 1 | | | 560 | | | | | |
| 35 | | | ,,, | | | | | 500 | | | | | |
| | a m a | ጠይጠ | CCA | ር <mark>አ</mark> ጥ | መመረ | GTG. | acc | a ጥር | GCC | RRR | GGG | መጥር | 1764 |
| | | | Pro | | | | | | | | | | 2,04 |
| 40 | | TÄT | FIO | wab | Ena | 570 | 7 11 T | 176 | WTO | пур | 575 | Euc | |
| | 565 | | | | | 570 | | | | | 3/3 | | |
| | | | | | | | | 2.00 | 22.5 | 224 | 00.0 | 4 555 | |
| | | | | | | | | | | | | GAA | 1800 |
| 45 | Asn | Ile | Pro | | Val. | Arg | Va1 | Thr | _ | Lys | asn | Glu | |
| | | | | 580 | | | | | 585 | | | | |
| | | | | | | | | | | | | | |
| 50 | GTC | CGC | GCA | GCG | ATA | AAG | AAG | ATG | CTC | GAG | act | CCA | 1836 |
| | Val | Arg | Ala | Ala | Ile | Lys | Lys | Met | Leu | Glu | Thr | Pro | |
| | | 590 | | | | | 595 | | | | | 600 | |

| | GGG | CCG | TAC | CTC | TTG | GAT | ATA | ATC | GTC | CCA | CAC | CAG | 1872 |
|----|------|------|------|------|------|-----|-----|-----|------------|-----|-----|-----|--------------|
| | Gly | Pro | Tyr | Leu | Leu | Asp | Ile | Ile | Val | Pro | His | Gln | |
| 5 | | | - | | 605 | | | | | 610 | | | |
| | | | | | | | | | | | | | |
| | GAG | CAT | GTG | TTG | CCT | ATG | ATC | CCT | AGT | GGT | GGG | GCT | 1908 |
| 10 | Glu | His | Val | Leu | Pro | Met | Ile | Pro | ser | Gly | Gly | Ala | |
| ,, | | | 615 | | | | | 620 | | | | | |
| | | | | | | | | | | | | | |
| | TTC | AAG | GAT | ATG | ATC | CTG | GAT | GGT | gat | GGC | AGG | act | 19 44 |
| 15 | Phe | Lys | Asp | Met | Ile | Leu | Asp | Gly | Asp | Gly | Arg | Thr | |
| | 625 | | | | | 630 | | | | | 635 | | |
| | | | | | | | | | | | | | |
| 20 | GTG | TAC | | | | | | | | | | | 1950 |
| | Val | Tyr | | | | | | | | | | | |
| | | 638 | | | | | | | | | | | |
| 25 | | | | | | | | | | | | | |
| | TGAT | CTAF | C AA | CCAC | CAAC | 3 | | | | | | | 1969 |
| | | | | | | | | | | | | | |
| 30 | | | | | | | | | | | | | |
| 30 | | | | | | | | | | | | | |
| | | | | | | | | | | | | | |
| | | | | | | | | | | | | | |
| 35 | | | | | | | | | | | | | |
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| 40 | | | | | | | | | | | | | |
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| | | | • | | | | | | | | | | |
| 45 | | | | | | | | | | | | | |
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| | | | | | | | | | | | | | |
| 50 | | | | | | | | | | | | | |
| 50 | | | | | | | | | | | | | |
| | | | | | | | | | | | | | |
| | | | | | | | | | | | | | |

| | Sequence ID No.: 3 | | |
|----|----------------------------------|------------------|-----|
| 5 | Sequence Type: Nucleotide and A | amino Acid | |
| 10 | Sequence Length: 1969 BP's and | 638 Amino Acids | |
| | Strandedness: Single | | |
| 15 | Topology: Linear | | |
| | Original Source Organism: Zea m | aays | • |
| 20 | Properties: Herbicide Sensitive | AHAS Enzyme | |
| 25 | | | |
| 25 | AACCCTCGCG CCGCCTCCGA GACAGCCGCC | : GCAACC | 36 |
| | ATG GCC ACC GCC GCC GCG TCT | ACC GCG CTC ACT | 72 |
| 30 | Met Ala Thr Ala Ala Ala Ala Ser | Thr Ala Leu Thr | |
| | 1 5 | 10 | |
| | GGC GCC ACT ACC GCT GCG CCC AAG | COC 3-CC CCC CCC | 108 |
| 35 | Gly Ala Thr Thr Ala Ala Pro Lys | | 100 |
| | 15 20 | are ary ary | |
| | | | |
| 40 | GCG CAC CTC CTG GCC ACC CGC CGC | GCC CTC GCC GCG | 144 |
| | Ala His Leu Leu Ala Thr Arg Arg | Ala Leu Ala Ala | |
| | 25 30 | 35 | |
| 45 | | | |
| | CCC ATC AGG TGC TCA GCG GCG TCA | | 180 |
| | Pro Ile Arg Cys Ser Ala Ala Ser | 45 | |
| 50 | 70 | | |
| | ATG GCT CCC CCG GCC ACC CCG CTC | CGG CCG TGG GGC | 216 |
| | Met Ala Pro Pro Ala Thr Pro Leu | Arg Pro Trp Gly | |
| 55 | 50 55 | 60 | |

| | CCC | ACC | GAG | CCC | CGC | AAG | GGT | GCT | GAC | atc | CTC | GTC | 252 |
|----|-----|-------|------|-------|------------------|-----|-------------|-----------------|--------------|------|-------|------------|-------------|
| 5 | Pro | Thr | Glu | Pro | Arg | Lys | Gly | Ala | Asp | Ile | Leu | Val | |
| | | | | | 65 | | | | | 70 | | | |
| | | | | | | | | | | | | | |
| 10 | GAG | TCC | CTC | GAG | CGC | TGC | GGC | GTC | CGC | GAC | GTC | TTC | 288 |
| | Glu | ser | Leu | Glu | Arg | Cys | Gly | ASI | Arg | Asp | ASI | Phe | |
| | | | 75 | | | | | 80 | | | | | |
| 15 | coo | ma 🗸 | 000 | ccc | ccc | ccc | MAG. | ^አ ምሮ | CRC | 2 MV | O R O | CAG | 324 |
| | | | | | | | | | Glu | | | | 324 |
| | 85 | ~ y ~ | r. U | GLY | G _Z y | 90 | | Mot | G Z G | 220 | 95 | 924 | |
| | | | | | | | | | | | | | |
| 20 | GCA | CTC | ACC | CGC | TCC | ccc | GTC | ATC | GCC | AAC | CAC | CTC | 360 |
| | Ala | Leu | Thr | Arg | Ser | Pro | v al | Ile | Ala | Asn | His | Leu | |
| | | | | 100 | | | | | 105 | | | | |
| 25 | | | | | | | | | | | | • | |
| | TTC | CGC | CAC | GAG | CAA | GGG | GAG | GCC | TTT | GCC | GCC | TCC | 396 |
| | Phe | Arg | His | Glu | Gln | Gly | Glu | Ala | Phe | Ala | Ala | Ser | |
| 30 | | 110 | | | | | 115 | | | | | 120 | |
| | | | | | | | | | | | | | |
| | GGC | TAC | GCG | CGC | TCC | TCG | GGC | CGC | GTC | GGC | GTC | TGC | 432 |
| 35 | Gly | Tyr | Ala | Arg | Ser | Ser | Gly | Arg | Val | Gly | A97 | Cys | |
| | | | | | 125 | | | | | 130 | | | |
| | | | | | | | | | | | | | |
| 40 | | | | | | | | | ACC | | | | 468 |
| | Ile | Ala | | Ser | GIĄ | Pro | Gly | | Thr | ASN | Leu | AST | |
| | | | 135 | | | | | 140 | | | | | |
| 45 | ሞሮሮ | GCG | ርጥር | GCC | GAC | GCG | ርጥਫ | ርሞር | GAT | TCC | GTC | ccc | 50 4 |
| | | | | | | | | | Asp | | | | |
| | 145 | 1124 | 200 | 252.6 | 2.06 | 150 | | | | | 155 | | |
| | 2.5 | | | | | | | | | | | | |
| 50 | ATG | GTC | GCC | ATC | ACG | GGA | CAG | GTG | CCG | CGA | CGC | ATG | 540 |
| | | | | | | | | | Pro | | | | |
| | | | | 160 | | - | | | 165 | _ | _ | | |
| 55 | | | | | | | | | | | | | |

| | att | GGC | ACC | GAC | GCC | TTC | CAG | GAG | ACG | CCC | atc | GTC | 576 |
|----|-----|------------|-----|------------|-----|------|-----|-----|-----|-----|------------|-----|-----|
| | Trp | Gly | Thr | Asp | Ala | Phe | Gln | Glu | Thr | Pro | Ile | AUI | |
| 5 | | 170 | | | | | 175 | | | | | 180 | |
| | GAG | GTC | ACC | CGC | TCC | ATC | ACC | AAG | CAC | AAC | TAC | CTG | 612 |
| | Glu | Val | Thr | Arg | ser | Ile | Thr | ras | His | Asn | Tyr | Leu | |
| 10 | | | | | 185 | | | | | 190 | | | |
| | GTC | CTC | GAC | GTC | GAC | GAC | ATC | ccc | CGC | GTC | GTG | CAG | 648 |
| 15 | Val | Leu | Asp | Ası | Asp | Asp | Ile | Pro | Arg | Asj | Avi | Gln | |
| | | | 195 | | | | | 200 | | | | | |
| 20 | GAG | GCT | TTC | TTC | CTC | GCC | TCC | TCT | GGT | CGA | CCA | GGG | 684 |
| | Glu | Ala | Phe | Phe | Leu | Ala | 8er | 8er | Gly | Arg | Pro | Gly | |
| | 205 | | | | | 210 | | | | | 215 | | |
| | | | | | | | | | | | | | |
| 25 | CCG | GTG | CTT | GTC | GAC | atc | ccc | AAG | GAC | atc | CAG | CAG | 720 |
| | Pro | Val | Leu | Asj | Asp | Ile | Pro | Lys | Asp | Ile | Gln | Gln | |
| | | | | 220 | | | | | 225 | | | | |
| 30 | | | | | | | | | | | | | |
| | CAG | ATG | GCG | GTG | CCT | GTC | TGG | GAC | AAG | CCC | atg | agt | 756 |
| | Gln | Met | Ala | Val | Pro | Val | Trp | Asp | Lys | Pro | Jem | Ser | |
| 05 | | 230 | | | | | 235 | | • | | | 240 | |
| 35 | | | | | | | | | | | | | |
| | CTG | CCT | GGG | TAC | ATT | GCG | CGC | CTT | ccc | AAG | ccc | CCT | 792 |
| | Leu | Pro | Gly | Tyr | Ile | Ala | Arg | Leu | Pro | Lys | Pro | Pro | |
| 40 | | | | | 245 | | | | | 250 | | | |
| | | | | | | | | | | | | | |
| | GCG | ACT | GAG | TTG | CTT | GAG | CAG | GTG | CTG | CGT | CTT | GTT | 828 |
| 45 | Ala | Thr | Glu | Leu | Leu | Glu | Gln | Asj | Leu | Arg | Leu | Val | |
| | | | 255 | | | | | 260 | | | | | |
| | | | | | | | | | | | | | |
| | GGT | GAA | TCG | CGG | CGC | CCT | GTT | CTT | TAT | GTG | GGC | GGT | 864 |
| 50 | Gly | Glu | Ser | Arg | Arg | Pro. | Val | Leu | Tyr | Val | Gly | Gly | |
| | 265 | | | _ | _ | 270 | | | | | 275 | | |

| | GCG | TGC | GCA | GCA | TCT | GGT | GAG | GAG | TTG | CGA | CGC | TTT | 900 |
|----|------|------|-------------|------|--------|-----|--------------|-----|-----|-----|-------|-----|------|
| | Ala | Cys | Ala | Ala | Ser | Gly | Glu | Glu | Leu | Arg | Arg | Phe | |
| 5 | | | | 280 | | | | | 285 | | | | |
| | | | | | | | | | | | | | |
| | GTG | GAG | CTG | ACT | GGA | ATC | CCG | GTC | ACA | ACT | ACT | CTT | 936 |
| | Val | Glu | Leu | Thr | Gly | Ile | Pro | Val | Thr | Thr | Thr | Leu | |
| 10 | | 290 | | | | | 295 | | | | | 300 | |
| | | | | | | | | | | | | | |
| | ATG | GGC | CTC | GGC | AAC | TTC | ccc | AGC | GAC | GAC | CCA | CTG | 972 |
| 15 | Met | Gly | Leu | Gly | Asn | Phe | Pro | Ser | Asp | Asp | Pro | Leu | |
| | | | | | 305 | | | | | 310 | | | |
| | | | | | | | | | | | | | |
| 20 | TCT | CTG | CGC | ATG | CTA | GGT | ATG | CAT | GGG | ACG | GTG | TAT | 1008 |
| | Ser | Leu | Arg | Met | Leu | Gly | Met | His | Gly | Thr | Val | Tyr | |
| | | | 315 | | | | | 320 | | | | | |
| 25 | | | | | | | | | | | | | |
| 25 | GCA | AAT | TAT | GCA | GTG | GAT | AAG | GCC | GAT | CTG | TTG | CTT | 1044 |
| | | Asn | Tyr | Ala | Val | Asp | Lys | Ala | Asp | Leu | | Leu | |
| | 325 | | | | | 330 | | | | | 335 | | |
| 30 | | | | | | | | | | | | | |
| | | | | | CGG | | | | | | | | 1080 |
| | Ala | Leu | Gly | | Arg | Phe | Asp | Asp | | Val | Thr | Gly | |
| 35 | | | | 340 | | | | | 345 | | | | |
| | | | | | | | | | | | | ama | |
| | | | | | TTT | | | | | | _ | _ | 1116 |
| 40 | rås | | GIU | ATA | Phe | AIA | | Arg | Ala | гÀа | 116 | 360 | |
| | | 350 | | | | | 355 | | | | | 300 | |
| | 03.0 | amm. | 63 m | 3.00 | C3 III | 000 | COM | CNC | 300 | ccc | 226 | AAC | 1152 |
| | | | | | Asp | | | | | | | | 1132 |
| 45 | піз | Val | Asp | 116 | 365 | PIO | WIG | GIU | 116 | 370 | DJS | nsu | |
| | | | | | 303 | | | | | 570 | | | |
| | 224 | CRC | CON | CAM | CTIC | ጥረረ | አ ጥ/ን | ጥረመ | GCA | СУТ | Gŵŵ | AAG | 1188 |
| 50 | | | | | Val | | | | | | | | 7100 |
| | гåа | GTU | | UTR | AGI | PEL | 116 | 380 | vid | vaħ | 4 G.I | ujo | |
| | | | 375 | | | | | 300 | | | | | |

| | CTT | GCT | TTG | CAG | GGC | ATG | AAT | GCT | CTT | ctt | gaa | GGA | 1224 |
|----|-----|-------|----------|-------------|-------------|-----------------|--------------|--------------|------|-------|--------|------|---------|
| | Leu | Ala | Leu | Gln | Gly | Met | Asn | Ala | Leu | Leu | Glu | Gly | |
| 5 | 385 | | | | | 390 | | | | | 395 | | |
| | | | | | | | | | | | | | |
| | AGC | ACA | TCA | AAG | AAG | AGC | TTT | GAC | TTT | GGC | TCA | TGG | 1260 |
| | Ser | Thr | ser | Lys | Lys | ser | Phe | Asp | Phe | Gly | 8er | Trp | |
| 10 | | | | 400 | | | | | 405 | | | | |
| | | | | | | | | | | | | | |
| | AAC | GAT | GAG | TTG | GAT | CAG | CAG | AAG | AGG | GAA | TTC | ccc | 1296 |
| 15 | Asn | Asp | Glu | Leu | Asp | Gln | Gln | Lys | Arg | Glu | Phe | Pro | |
| | | 410 | | | _ | | 415 | | _ | | | 420 | |
| | | | | | | | | | | | | | |
| 20 | CTT | GGG | TAT | AAA | ACA | TCT | AAT | GAG | GAG | ATC | CAG | CCA | 1332 |
| 20 | | | Tyr | | | | | | | | | | |
| | | 2 | -4- | -3 | 425 | | | | | 430 | | | |
| | | | | | | | | | | | | | |
| 25 | CAA | ጥኤጥ | GCT | ኤ ጥጥ | CAG | ር ጥጥ | ርምም | ር ይጥ | GAG | ርጥਫ | ace. | AAA | 1368 |
| | | | Ala | | | | | | | | | | 2000 |
| | GLM | * % * | 435 | 440 | 4 | V & A. | 200 | 440 | GZG | 204 | 2 24 2 | ay s | |
| 30 | | | 433 | | | | | 440 | | | | | |
| | 000 | CPC | coo | »ma | 2 m/v | cco | 2 0 2 | CCM | ~mm | ccc | OB C | CAC | 1404 |
| | | | | | | | | | | | | _ | 2000 |
| | • | GIU | Ala | TTR | TIG | | THE | GIÀ | AFIT | GIY | 455 | urs | |
| 35 | 445 | | | | | 450 | | | | | ขออ | | |
| | | | | | 5 50 | | 550 | 550 6 | 5.69 | 530 A | 55.69 | | 9 4 4 8 |
| | | | TGG _ | | | | | | | | | | 1440 |
| 40 | Gln | Met | Trp | | Ala | Gln | ryr | TYT | | TYT | гàз | Arg | |
| | | | | 460 | | | | | 465 | | | | |
| | | | | | | | | | | | | | |
| | | | CAG | | | | | | | | | | 1476 |
| 45 | Pro | Arg | Gln | Trp | Leu | Ser | ser | Ala | Gly | Leu | Gly | Ala | |
| | | 470 | | | | | 475 | | | | | 480 | |
| | | | | | | | | | | | | | |
| 50 | ATG | GGA | TTT | GGT | TTG | CCG | GCT | GCT | GCT | GGT | GCT | TCT | 1512 |
| | Met | Gly | Phe | Gly | Leu | Pro | Ala | Ala | Ala | Gly | Ala | ser | |
| | | | | | 485 | | | | | 490 | | | |

| 5 | GTG | GCC | AAC | CCA | GGT | GTC | act | GTT | GTT | GAC | ATC | GAT | 1548 |
|----|-------|------------|------------|-------------|-----|------|-----------|----------------------|-------|------------|------|--------------|--------------|
| v | Val | Ala | Asn | Pro | Gly | Val | Thr | val | asi | Asp | Ile | Asp | |
| | | | 495 | | | | | 500 | | | | | |
| | | | | | | | | | | | | | |
| 10 | GGA | GAT | GGT | AGC | TTT | CTC | atg | AAC | GTT | CAG | GAG | CTA | 158 4 |
| | Gly | Asp | Gly | Ser | Phe | Leu | Met | Asn | Val | Gln | Glu | Leu | |
| | 505 | | | | | 510 | | | | | 515 | | |
| 15 | | | | | | | | | | | | | |
| | GCT | atg | atc | CGA | ATT | GAG | AAC | CTC | CCA | GTG | aag | GTC | 1620 |
| | Ala | Met | Ile | Arg | Ile | Glu | Asn | Leu | Pro | Asj | råa | Val | |
| 20 | | | | 520 | | | | | 525 | | | | |
| | | | | | | | | | | | | | |
| | TTT | GTG | CTA | AAC | AAC | CAG | CAC | CTG | GGG | ATG | GTG | GTG | 1656 |
| | Phe | Val | Leu | Asn | Asn | Gln | His | Leu | Gly | Met | val | | |
| 25 | | 530 | | | | | 535 | | | | | 540 | |
| | | | | | | | | | | | | | |
| | | | | | | | | | | | | GCG | 1692 |
| 30 | Gln | Trp | Glu | Asp | - | Phe | Tyr | Lys | Ala | | Arg | Ala | |
| | | | | | 545 | | | | | 550 | | | |
| | | D | | | 885 | 22.0 | ~~ | ~ 5~ ~ | 0.089 | 455 | 5.45 | 4 5.4 | 8700 |
| 35 | | | | | | | | | | | | GAG | 1728 |
| | nıs | Tur | Tyr 555 | าลถ | GIÀ | ASII | BTO | 560 | ASII | GIU | Par | GLU | |
| | | | 333 | | | | | 300 | | | | | |
| 40 | מידים | ጥይጥ | CCA | ር ልጥ | ጥጥሮ | GTG | a.c.c | a ጥር | GCC | 24.24.24 | GGG | ጥጥር | 1764 |
| | | | Pro | | | | | | | | | | 2.00 |
| | 565 | - 1 - | | 2300 | • | 570 | | | | | 575 | | |
| 45 | 303 | | | | | | | | | | | | |
| 45 | AAC | ATT | CCA | GCG | GTC | CGT | GTG | ACA | AAG | AAG | AAC | GAA | 1800 |
| | | | Pro | | | | | | | | | | |
| | | | | 580 | | | | | 585 | - | | | |
| 50 | | | | | | | | | | | | | |
| | GTC | CGC | GCA | GCG | ATA | AAG | AAG | ATG | CTC | GAG | ACT | CCA | 1836 |
| | | | Ala | | | | | | | | | | |
| 55 | | 590 | | | | _ | 595 | | | | | 600 | |
| | | | | | | | | | | | | | |

| | GGG | CCG | TAC | CTC | TTG | GAT | ATA | ATC | GTC | CCA | CAC | CAG | 1872 |
|----|------|------|-------|------|------|-----|-----|-----|------------|-----|-----|-----|------|
| 5 | Gly | Pro | Tyr | Leu | Leu | Asp | Ile | Ile | Val | Pro | His | Gln | |
| | | | | | 605 | | | | | 610 | | | |
| | | | | | | | | | | | | | |
| 10 | GAG | CAT | GTG | TTG | CCT | ATG | ATC | CCT | agt | GGT | GGG | GCT | 1908 |
| 70 | Glu | His | Val | Leu | Pro | Met | Ile | Pro | ser | Gly | Gly | Ala | |
| | | | 615 | | | | | 620 | | | | | |
| | | | | | | | | | | | | | |
| 15 | TTC | AAG | gat | ATG | ATC | CTG | gat | GGT | gat | GGC | AGG | act | 1944 |
| | Phe | Lys | Asp | Met | Ile | Leu | Asp | Gly | Asp | Gly | Arg | Thr | |
| | 625 | | | | | 630 | | | | | 635 | | |
| 20 | | | | | | | | | | | | | |
| | GTG | TAC | | | | | | | | | | | 1950 |
| | va1 | Tyr | | | | | | | | | | | |
| | | 638 | | | | | | | | | | | |
| 25 | | | | | | | | | | | | | |
| | TGAT | CTAI | laa 1 | CCAC | CAAC | 3 | | | | | | | 1969 |

Claims

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1. A monocot nucleic acid sequence encoding a functional AHAS enzyme, which enzyme has an amino acid substitution relative to a wild-type monocot AHAS enzyme, and which substitution confers imidazolinone-specific resistance to the enzyme.

- 2. The sequence of Claim 1 in which the monocot is corn and the substitution is at position 621 in the wild-type corn AHAS enzyme.
- 3. The sequence of Claim 2 in which the substituted amino acid is asparagine.
- 4. A functional monocot AHAS enzyme which has an amino acid substitution relative to a monocot wild-type AHAS enzyme, and which substitution confers imidazolinone-specific resistance to the enzyme.
- 5. The enzyme of Claim 4 in which the monocot is corn and the substitution is at position 621 in the wildtype corn AHAS enzyme.
- 6. The enzyme of Claim 5 in which the substituted amino acid is asparagine.
- 7. A transformation vector comprising the nucleic acid of Claim 1.
- 8. A host cell comprising the nucleic acid sequence of Claim 1, or the vector of Claim 7.
- 55 9. The host cell of Claim 8 which is a plant cell or a bacterial cell.
 - 10. An imidazolinone-specific resistant mature plant containing the nucleic acid sequence of Claim 1, or seed or pollen therefrom.

- 11. A method of conferring imidazolinone-specific resistance to a plant cell which comprises providing the plant cell with the nucleic acid sequence of Claim 1.
- 12. A method for growing imidazolinone-specific resistant plants which comprises cultivating a plant which produces the enzyme of Claim 4 in the presence of an inhibitory amount of imidazolinone.
 - 13. A method of selecting host cells successfully transformed with a gene of interest which comprises providing to prospective host cells the gene of interest linked to the nucleic acid sequence of Claim 1, or unlinked but in the presence of the nucleic acid sequence of Claim 1, growing the cells in the presence of an inhibitory amount of imidazolinone and identifying surviving cells as containing the gene of interest.
- 14. A nucleic acid construct comprising the sequence of Claim 1 linked to a gene encoding an agronomically useful trait.

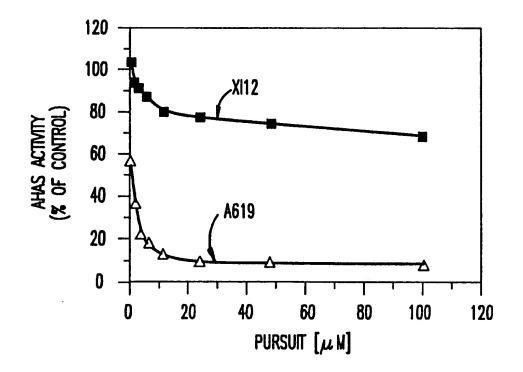


FIG.1A

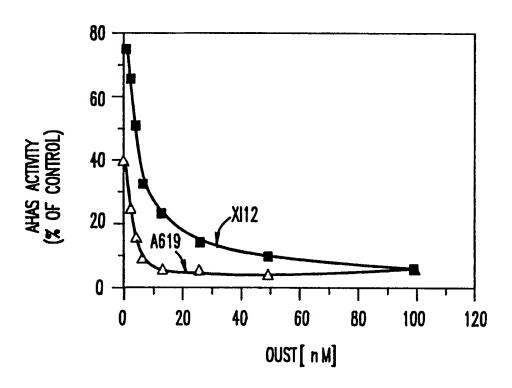
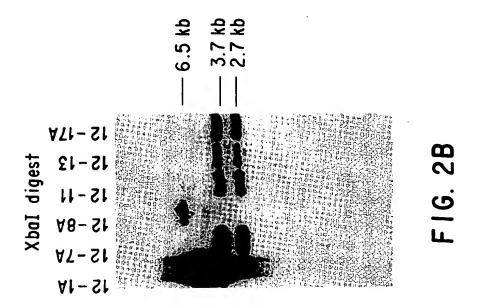
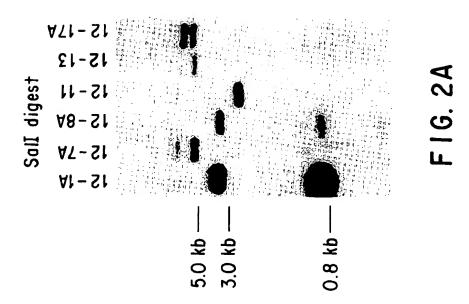


FIG.1B





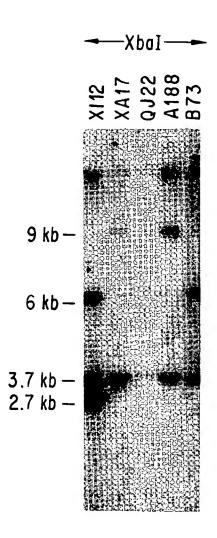
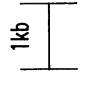
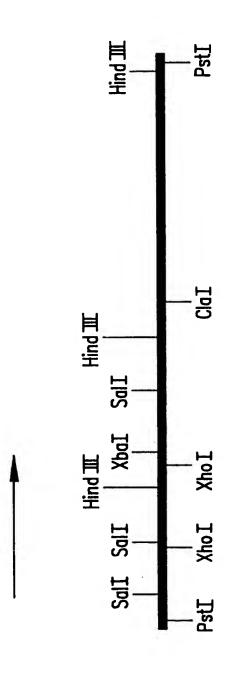


FIG. 3





-16.4

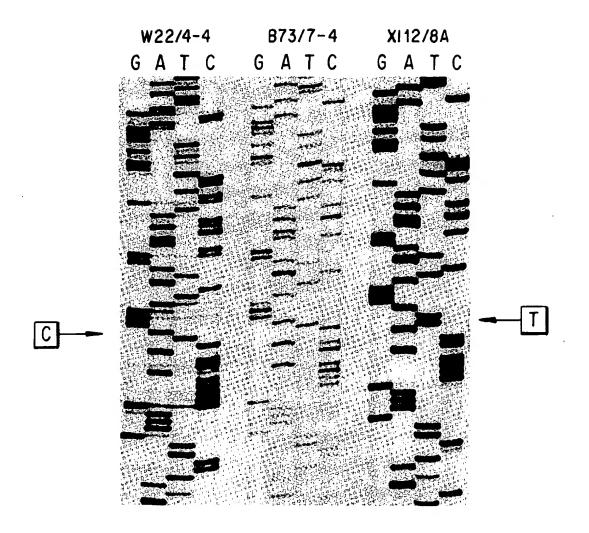


FIG. 5A

W22/1A and B73/7-4

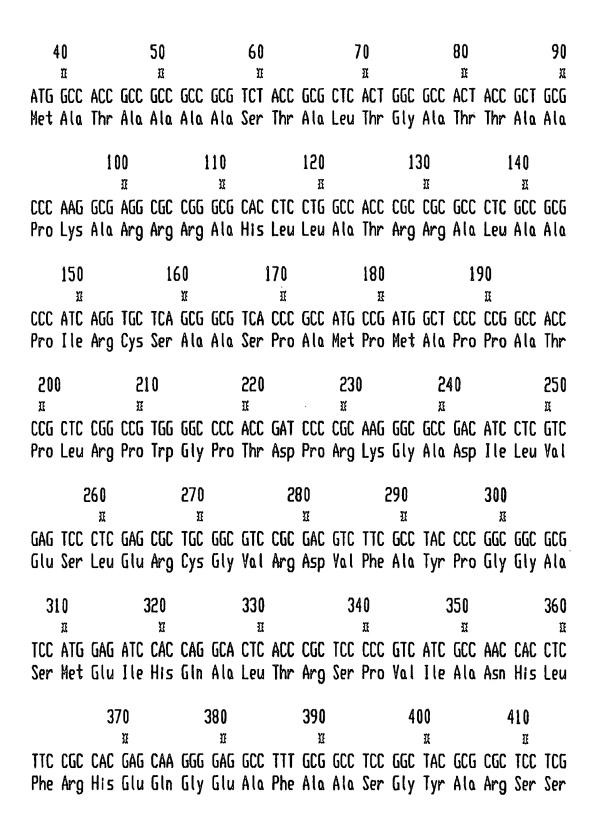
5'TAGTG3' 3'ATCTG5'

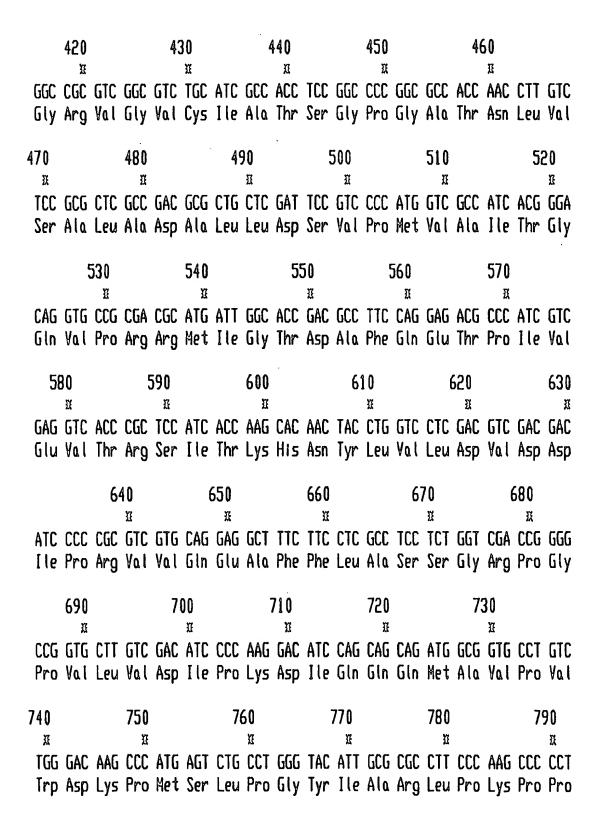
sequence:

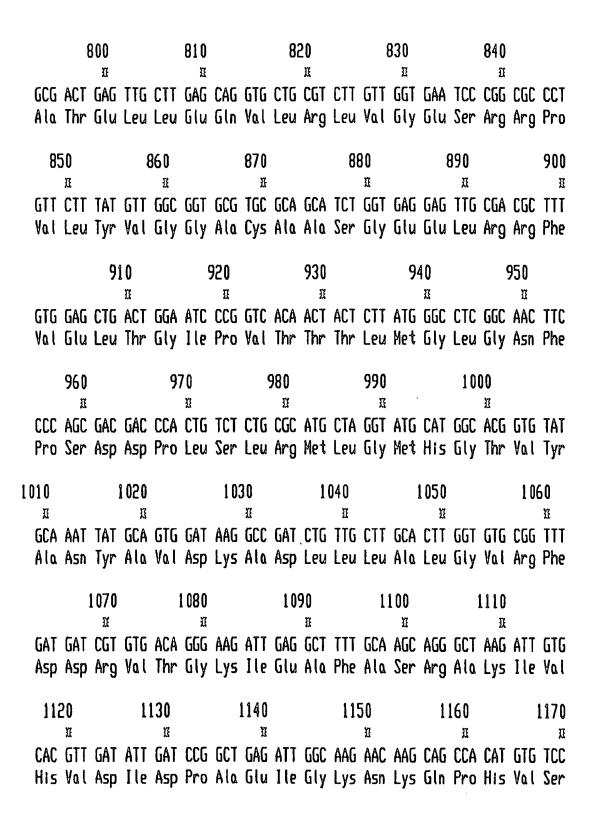
XI12/8A sequence:

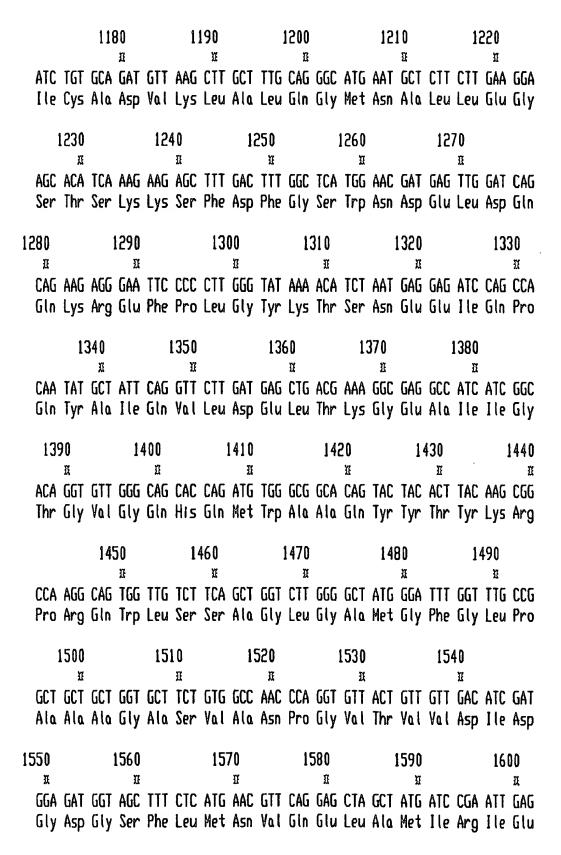
5'TAATG3' 3'ATTAC5'

F1G. 5B









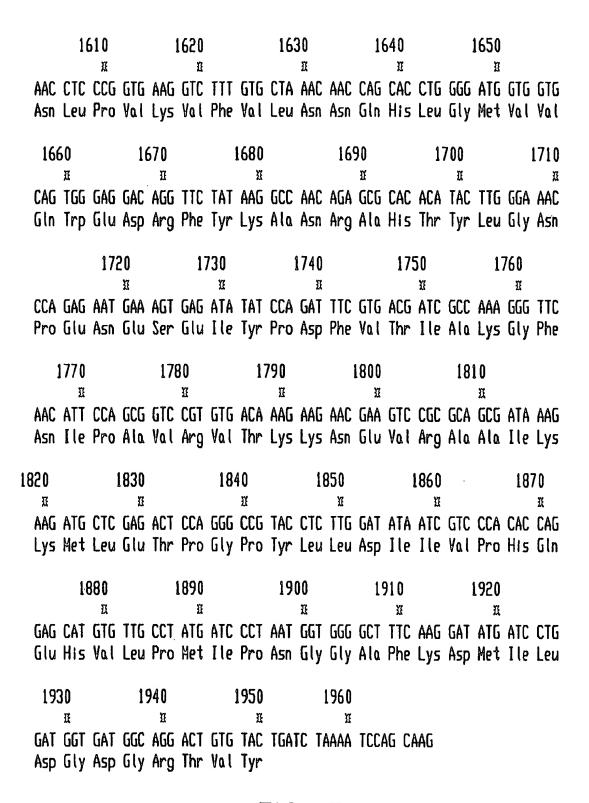


FIG.6E

| | | 10 | | 20 | | 30 | | 40 | | 50 | | 60 |
|----------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-----------|
| X112/8A | AACCC | TCGCG | CCGCC | TCCGA | GACAG | CCGCC | GCAAC | CATGG | CCACC | GCCGC | CGCCG | CGTCT |
| ¥22/1A | | TCGCG | | | | | | | | | | |
| | | 11111 | | | | | | | | | | |
| B73/7-4 | | TCGCG | | | | | | | | | | |
| | | 11111 | | | | | | | | | | |
| XI12/8A | AACCC | TCGCG | CCGCC | TCCGA | GACAG | CCGCC | GCAAC | CATGG | CCACC | GCCGC | CGCCG | CGTCT |
| | | 70 | | 80 | | 90 | | 100 | | 110 | | 120 |
| XI12/8A | ACCGC | GCTCA | CTGGC | GCCAC | TACCG | CTGCG | CCCAA | GGCGA | GGCGC | CGGGC | GCACC | TCCTG |
| | | | | | | | | | | | | |
| A55/19 | | GCTCA | | | | | | | | | | |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
| B73/7-4 | ACCGC | GCTCA | CTGGC | GCCAC | TACCG | CTGCG | CCCAA | GGCGA | GGCGC | CGGGC | GCACC | TCCTG |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
| XI12/8A | | GCTCA | | | | | | | | | | |
| | | | | | | | | | | | | |
| | | | | 140 | | | | | | | | |
| XI12/8A | GCCAC | CCGCC | GCGCC | CTCGC | CGCGC | CCATC | AGGTG | CTCAG | CGGCG | TCACC | CGCCA | TGCCG |
| H22/1A | GCCAC | CCGCC | GCGCC | CTCGC | CECEC | CCATC | AGGTG | CTCAG | CEECE | TOACE | LLLLV | TECCE |
| | | 11111 | | | | | | | | | | |
| B73/7-4 | | CCGCC | | | | | | | | | | |
| <i>D. G. i</i> | | 11111 | | | | | | | | | | |
| X112/8A | | CCGCC | | | | | | | | | | |
| ATTE/ UN | GOUNG | CUGGG | dodoo | CICUC | LUCUL | CUNIC | nuulu | CICHU | Caaca | TONOL | LUCCH | 10000 |
| | | 190 | | 500 | | 210 | | 550 | | 230 | | 240 |
| A8/S11X | ATGGC | TCCCC | CGGCC | ACCCC | GCTCC | GGCCG | TGGGG | CCCCA | CCGAT | CCCCG | CAAGG | GCGCC |
| | | | | | | | | | # | | | 〉〉 |
| A55\1V | ATGGC | TCCCC | CGGCC | ACCCC | GCTCC | GGCCG | TGGGG | CCCCA | CCGAT | CCCCG | CAAGG | GCGCC |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 1111 | 11111 | 11111 | 1 11 |
| B73/7-4 | ATGGC | TCCCC | CGGCC | ACCCC | GCTCC | GGCCG | TGGGG | CCCCA | CCGAg | CCCCG | CAAGG | GtGCt |
| | | 11111 | | | | | | | | | | |
| X112/8A | | | CGGCC | | | | | | | | | |

| | | 250 | | | | | | | | | | 300 |
|---------------------------------------|---|---|---|---|---|--|---|---|--|---|---|--|
| X112/8A | GACAT | CCTCG | TCGAG | TCCCT | CGAGC | GCTGC | GGCGT | CCGCG | ACGTC | TTCGC | CTACC | CCGGC |
| H22/1A | | | TCGAG | | | | | | | | | |
| | | | 11111 | | | | | | | | | |
| B73/7-4 | | | TCGAG | | | | | | | | | |
| | | | 11111 | | | | | | | | | |
| XI12/8A | GACAT | CCICL | TCGAG | ICCCI | CUAUC | ULTUL | <u> Մ</u> | LLULU | ALUIL | HUUL | LIALL | lluul |
| | | 310 | | | | | | | | | | 360 |
| X112/8A | GGCGC | GTCCA | TGGAG | ATCCA | CCAGG | CACTC | ACCCG | CTCCC | CCGTC | ATCGC | CAACC | ACCTC |
| 422/1A | GGCGC | GTCCA | TGGAG | ATCCA | CCAGG | CACTC | ACCCG | CTCCC | CCGTC | ATCGC | CAACC | ACCTC |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
| XB73/7-4 | | | TGGAG | | | | | | | | | |
| | | | 11111 | | | | | | | | | |
| X112/8A | GGCGC | GTCCA | TGGAG | ATCCA | CCAGG | CACTC | ACCCG | CTCCC | CCGTC | ATCGC | CAACC | ACCTC |
| | | | | | | | | | | | | |
| | | 370 | | 380 | | 390 | | 400 | | 410 | | 420 |
| X112/8A | TTCCG | | AGCAA | | | | | | | | | |
| | | CCACG | AGCAA | GGGGA | GGCCT | TTGCG > | GCCTC | CGGCT | ACGCG | CGCTC | CTCGG | GCCGC |
| X112/8A V22/1A | TTCCG | CCACG CCACG | AGCAA | GGGGA GGGGA | GGCCT GGCCT | TTGCG > | GCCTC GCCTC | CGGCT CGGCT | ACGCG ACGCG | CGCTC | CTCGG CTCGG | GCCGC |
| ¥22/1A | TTCCG 11111 | CCACG CCACG 11111 | AGCAA 11111 | GGGGA 11111 | GGCCT 11111 | TTGCG > TTGCG | GCCTC GCCTC 11111 | CGGCT CGGCT 11111 | ACGCG ACGCG 11111 | CGCTC CGCTC 11111 | CTCGG 11111 | GCCGC 11111 |
| | TTCCG 11111 TTCCG 11111 | CCACG 11111 CCACG 11111 | AGCAA 11111 AGCAA 11111 | GGGGA 11111 GGGGA 11111 | GGCCT 11111 GGCCT 11111 | TTGCG | GCCTC GCCTC 11111 GCCTC 11111 | CGGCT 11111 CGGCT 11111 | ACGCG 11111 ACGCG 11111 | CGCTC 11111 CGCTC 11111 | CTCGG 11111 CTCGG 11111 | GCCGC 11111 GCCGC 11111 |
| ¥22/1A | TTCCG 11111 TTCCG 11111 | CCACG 11111 CCACG 11111 | AGCAA 11111 AGCAA | GGGGA 11111 GGGGA 11111 | GGCCT 11111 GGCCT 11111 | TTGCG | GCCTC GCCTC 11111 GCCTC 11111 | CGGCT 11111 CGGCT 11111 | ACGCG 11111 ACGCG 11111 | CGCTC 11111 CGCTC 11111 | CTCGG 11111 CTCGG 11111 | GCCGC 11111 GCCGC 11111 |
| W22/1A B73/7-4 | TTCCG 11111 TTCCG 11111 | CCACG 11111 CCACG 11111 | AGCAA 11111 AGCAA 11111 AGCAA | GGGGA 11111 GGGGA 11111 GGGGA | GGCCT 11111 GGCCT 11111 GGCCT | TTGCG TTGCG 1111 TTGCc 1111 TTGCG | GCCTC 11111 GCCTC 11111 GCCTC | CGGCT 11111 CGGCT 11111 CGGCT | ACGCG 11111 ACGCG 11111 ACGCG | CGCTC 11111 CGCTC 11111 CGCTC | CTCGG 11111 CTCGG 11111 CTCGG | GCCGC 11111 GCCGC 11111 |
| W22/1A B73/7-4 | TTCCG 11111 TTCCG 11111 TTCCG | CCACG 11111 CCACG 11111 CCACG 430 | AGCAA 11111 AGCAA 11111 AGCAA | GGGGA 11111 GGGGA 11111 GGGGA 440 | GGCCT 11111 GGCCT 11111 GGCCT | TTGCG TTGCG 1111 TTGCc 1111 TTGCG 450 | GCCTC 11111 GCCTC 11111 GCCTC | CGGCT CGGCT 11111 CGGCT 11111 CGGCT 460 | ACGCG 11111 ACGCG 11111 ACGCG | CGCTC 11111 CGCTC 11111 CGCTC 11111 CGCTC 470 | CTCGG 11111 CTCGG 11111 CTCGG | GCCGC 11111 GCCGC 11111 GCCGC 480 |
| W22/1A B73/7-4 XI12/8A | TTCCG 11111 TTCCG 11111 TTCCG | CCACG 11111 CCACG 11111 CCACG 430 CGTCT | AGCAA 11111 AGCAA 11111 AGCAA GCATC | GGGGA 11111 GGGGA 11111 GGGGA 440 GCCAC | GGCCT 11111 GGCCT 11111 GGCCT CTCCG | TTGCG TTGCG 1111 TTGCc 1111 TTGCG 450 GCCCC | GCCTC 11111 GCCTC 11111 GCCTC GCCTC | CGGCT CGGCT 11111 CGGCT 11111 CGGCT 460 CACCA | ACGCG 11111 ACGCG 11111 ACGCG ACGCG ACCTT | CGCTC 11111 CGCTC 11111 CGCTC 470 GTCTC | CTCGG 11111 CTCGG 11111 CTCGG | GCCGC GCCGC 11111 GCCGC 11111 GCCGC 480 TCGCC |
| W22/1A B73/7-4 XI12/8A XI12/8A | TTCCG 11111 TTCCG 11111 TTCCG GTCGG | CCACG 11111 CCACG 11111 CCACG 430 CGTCT | AGCAA 11111 AGCAA 11111 AGCAA | GGGGA 11111 GGGGA 11111 GGGGA 440 GCCAC | GGCCT GGCCT HIHH GGCCT HIHH GGCCT CTCCG | TTGCG | GCCTC GCCTC 11111 GCCTC 11111 GCCTC GGCGC GGCGC | CGGCT CGGCT 11111 CGGCT 11111 CGGCT 460 CACCA | ACGCG 11111 ACGCG 11111 ACGCG ACGCTT ACCTT ACCTT | CGCTC CGCTC 11111 CGCTC 11111 CGCTC 470 GTCTC | CTCGG 11111 CTCGG 11111 CTCGG | GCCGC GCCGC 11111 GCCGC 11111 GCCGC 480 TCGCC |
| W22/1A B73/7-4 XI12/8A XI12/8A | TTCCG 11111 TTCCG 11111 TTCCG GTCGG 11111 | CCACG 11111 CCACG 11111 CCACG 430 CGTCT CGTCT | AGCAA AGCAA 11111 AGCAA 11111 AGCAA GCATC | GGGGA 11111 GGGGA 11111 GGGGA 440 GCCAC GCCAC | GGCCT 11111 GGCCT 11111 GGCCT CTCCG CTCCG 11111 | TTGCG | GCCTC 11111 GCCTC 11111 GCCTC GGCGC GGCGC 11111 | CGGCT 11111 CGGCT 11111 CGGCT 460 CACCA CACCA | ACGCG 11111 ACGCG 11111 ACGCG ACCTT ACTT 1111 | CGCTC 11111 CGCTC 11111 CGCTC 470 GTCTC GTCTC 11111 | CTCGG 11111 CTCGG 11111 CTCGG CGCGC CGCGC | GCCGC GCCGC HIHH GCCGC HIHH GCCGC TCGCC HIHH |
| W22/1A B73/7-4 XI12/8A XI12/8A W22/1A | TTCCG 11111 TTCCG 11111 TTCCG GTCGG 11111 GTCGG 11111 | CCACG 11111 CCACG 11111 CCACG 11111 CCACG 430 CGTCT 11111 CGTCT 11111 | AGCAA AGCAA 11111 AGCAA 11111 AGCAA GCATC GCATC 11111 GCATC 11111 | GGGGA 11111 GGGGA 11111 GGGGA 440 GCCAC GCCAC 11111 GCCAC 11111 | GGCCT 11111 GGCCT 11111 GGCCT CTCCG CTCCG 11111 CTCCG 11111 | TTGCG TTGCG 1111 TTGCc 1111 TTGCG 450 GCCCC 11111 GCCCC 111111 | GCCTC 11111 GCCTC 11111 GCCTC GGCGC GGCGC 11111 GGCGC 11111 | CGGCT 11111 CGGCT 11111 CGGCT 460 CACCA CACCA 11111 CACCA 11111 | ACGCG 11111 ACGCG 11111 ACGCG ACCTT ACTT 1111 ACCTA 1111 | CGCTC 11111 CGCTC 11111 CGCTC 470 GTCTC 11111 GTCTC 11111 | CTCGG 11111 CTCGG 11111 CTCGG CGCGC CGCGC 11111 CGCGG 11111 | GCCGC 11111 GCCGC 11111 GCCGC 480 TCGCC TCGCC 11111 TCGCC |

| | | 490 | | 500 | | 510 | | 520 | | 530 | | 540 |
|---------------------------------------|---|---|---|---|---|---|---|--|--|---|---|---|
| XI12/8A | GACGC | GCTGC | TCGAT | TCCGT | CCCCA | TGGTC | GCCAT | CACGG | GACAG | GTGCC | GCGAC | GCATG |
| W22/1A | | | | TCCGT | | | | | | | | |
| | | | | 11111 | | | | | | | | |
| B73/7-4 | | | | TCCGT | | | | | | | | |
| | | | | 11111 | | | _ | | | | | |
| XI12/8A | GACGC | GCTGC | TCGAT | TCCGT | CCCCA | IGGIC | GCCAT | CACGG | GACAG | GIGCC | GCGAC | GEATG |
| | | 550 | | 560 | | 570 | | 580 | | 590 | | 600 |
| XI12/8A | ATTGG | | | TTCCA | | | | | | | | |
| | | | | | | | | | | | | |
| H25/19 | ATTGG | CACCG | ACGCC | TTCCA | GGAGA | CCCCC | ATCGT | CGAGG | TCACC | CGCTC | CATCA | CCAAG |
| | | | | 11111 | | | | | | | | |
| B73/7-4 | | | | TTCCA | | | | | | | | |
| | | | | 11111 | | | | | | | | |
| XI12/8A | ATTGG | CACCG | ACGCC | TTCCA | GGAGA | CECCC | ATCGT | CGAGG | TCACC | CGCTC | CATCA | CCAAG |
| | | | | | | | | | | | | |
| | | 610 | | 620 | • | 630 | | 640 | | 650 | | 660 |
| YI12/8A | ልልግልግ | | | 059 47171 | | | | | | | | |
| XI12/8A | CACAA | | | 620 CTCGA | | | | | | | | |
| XI12/8A V22/1A | | CTACC | TGGTC | | CGTCG | ACGAC | ATCCC | CCGCG | TCGTG | CAGGA | GGCTT | TCTTC |
| | CACAA | CTACC CTACC | TGGTC | CTCGA | CGTCG CGTCG | ACGAC ACGAC | ATCCC ATCCC | CCGCG | TCGTG TCGTG | CAGGA CAGGA | GGCTT GGCTT | TCTTC TCTTC |
| | CACAA 11111 | CTACC CTACC 11111 | TGGTC TGGTC 11111 | CTCGA CTCGA | CGTCG CGTCG 11111 | ACGAC 11111 | ATCCC 11111 | CCGCG 11111 | TCGTG TCGTG 11111 | CAGGA CAGGA 11111 | GGCTT GGCTT 11111 | TCTTC TCTTC 11111 |
| V22/1A | CACAA 11111 CACAA 11111 | CTACC 11111 CTACC 11111 | TGGTC 11111 TGGTC 11111 | CTCGA CTCGA 11111 CTCGA 11111 | CGTCG 11111 CGTCG 11111 | ACGAC 11111 ACGAC 11111 | ATCCC 11111 ATCCC 11111 | CCGCG 11111 CCGCG 11111 | TCGTG TCGTG 11111 TCGTG 11111 | CAGGA CAGGA 11111 CAGGA 11111 | GGCTT 11111 GGCTT 11111 | TCTTC TCTTC 11111 TCTTC 11111 |
| V22/1A | CACAA 11111 CACAA 11111 | CTACC 11111 CTACC 11111 | TGGTC 11111 TGGTC 11111 | CTCGA CTCGA 11111 CTCGA | CGTCG 11111 CGTCG 11111 | ACGAC 11111 ACGAC 11111 | ATCCC 11111 ATCCC 11111 | CCGCG 11111 CCGCG 11111 | TCGTG TCGTG 11111 TCGTG 11111 | CAGGA CAGGA 11111 CAGGA 11111 | GGCTT 11111 GGCTT 11111 | TCTTC TCTTC 11111 TCTTC 11111 |
| ¥22/1A B73/7-4 | CACAA 11111 CACAA 11111 | CTACC 11111 CTACC 11111 CTACC | TGGTC 11111 TGGTC 11111 TGGTC | CTCGA CTCGA 11111 CTCGA 11111 CTCGA | CGTCG CGTCG 11111 CGTCG 11111 CGTCG | ACGAC 11111 ACGAC 11111 ACGAC | ATCCC 11111 ATCCC 11111 ATCCC | CCGCG 11111 CCGCG 11111 CCGCG | TCGTG TCGTG 11111 TCGTG 11111 TCGTG | CAGGA 11111 CAGGA 111111 CAGGA | GGCTT 11111 GGCTT 11111 GGCTT | TCTTC 11111 TCTTC 11111 TCTTC |
| V22/1A B73/7-4 XI12/8A | CACAA 11111 CACAA 11111 CACAA | CTACC 11111 CTACC 11111 CTACC 670 | TGGTC 11111 TGGTC 11111 TGGTC 11111 TGGTC | CTCGA CTCGA 11111 CTCGA 11111 CTCGA 680 | CGTCG CGTCG 11111 CGTCG 11111 CGTCG | ACGAC 11111 ACGAC 11111 ACGAC 690 | ATCCC 11111 ATCCC 11111 ATCCC | CCGCG CCGCG 11111 CCGCG 11111 CCGCG 700 | TCGTG TCGTG 11111 TCGTG 11111 TCGTG | CAGGA CAGGA 11111 CAGGA 11111 CAGGA 710 | GGCTT 11111 GGCTT 11111 GGCTT | TCTTC 11111 TCTTC 11111 TCTTC 720 |
| ¥22/1A B73/7-4 | CACAA 11111 CACAA 11111 CACAA | CTACC 11111 CTACC 11111 CTACC 670 | TGGTC 11111 TGGTC 11111 TGGTC 11111 TGGTC | CTCGA CTCGA 11111 CTCGA 11111 CTCGA 680 | CGTCG CGTCG 11111 CGTCG 11111 CGTCG | ACGAC 11111 ACGAC 11111 ACGAC 690 | ATCCC 11111 ATCCC 11111 ATCCC | CCGCG CCGCG 11111 CCGCG 11111 CCGCG 700 | TCGTG TCGTG 11111 TCGTG 11111 TCGTG | CAGGA CAGGA 11111 CAGGA 11111 CAGGA 710 | GGCTT 11111 GGCTT 11111 GGCTT | TCTTC 11111 TCTTC 11111 TCTTC 720 |
| V22/1A B73/7-4 XI12/8A | CACAA 11111 CACAA 11111 CACAA | CTACC 11111 CTACC 11111 CTACC 11111 CTACC 670 CTCCT | TGGTC 11111 TGGTC 11111 TGGTC 11111 TGGTC CTGGT | CTCGA CTCGA 11111 CTCGA 11111 CTCGA 680 | CGTCG CGTCG 11111 CGTCG 11111 CGTCG GGGGC > | ACGAC 11111 ACGAC 11111 ACGAC 690 CGGTG | ATCCC ATCCC 11111 ATCCC 11111 ATCCC CTTGT | CCGCG CCGCG 11111 CCGCG 11111 CCGCG 700 CGACA | TCGTG TCGTG 11111 TCGTG 11111 TCGTG TCCCC | CAGGA 11111 CAGGA 11111 CAGGA 710 AAGGA | GGCTT 11111 GGCTT 11111 GGCTT CATCC | TCTTC 11111 TCTTC 11111 TCTTC 720 AGCAG |
| W22/1A B73/7-4 X112/8A X112/8A | CACAA 11111 CACAA 11111 CACAA CTCGC | CTACC 11111 CTACC 11111 CTACC 670 CTCCT | TGGTC 11111 TGGTC 11111 TGGTC CTGGT CTGGT | CTCGA CTCGA 11111 CTCGA 11111 CTCGA 680 CGACC | CGTCG CGTCG 11111 CGTCG 11111 CGTCG GGGGC GGGGC GGGGC | ACGAC 11111 ACGAC 11111 ACGAC 690 CGGTG | ATCCC 11111 ATCCC 11111 ATCCC CTIGT | CCGCG 11111 CCGCG 11111 CCGCG 700 CGACA | TCGTG TCGTG 11111 TCGTG 11111 TCGTG TCCCC TCCCC | CAGGA 11111 CAGGA 11111 CAGGA 710 AAGGA | GGCTT 11111 GGCTT 11111 GGCTT CATCC CATCC | TCTTC 11111 TCTTC 11111 TCTTC 720 AGCAG AGCAG |
| W22/1A B73/7-4 X112/8A X112/8A | CACAA 11111 CACAA 11111 CACAA CTCGC CTCGC 11111 | CTACC 11111 CTACC 11111 CTACC 670 CTCCT CTCCT | TGGTC 11111 TGGTC 11111 TGGTC CTGGT CTGGT 11111 | CTCGA CTCGA 11111 CTCGA 11111 CTCGA 680 CGACC | CGTCG 11111 CGTCG 11111 CGTCG CGTCG GGGGC GGGGC 11111 | ACGAC 11111 ACGAC 11111 ACGAC 690 CGGTG CGGTG 11111 | ATCCC ATCCC 11111 ATCCC 11111 ATCCC CTTGT CTTGT 11111 | CCGCG CCGCG 11111 CCGCG 11111 CCGCG 700 CGACA CGACA 11111 | TCGTG 11111 TCGTG 11111 TCGTG TCCCC TCCCC 11111 | CAGGA 11111 CAGGA 11111 CAGGA 710 AAGGA AAGGA 11111 | GGCTT 11111 GGCTT 11111 GGCTT CATCC CATCC 11111 | TCTTC 11111 TCTTC 11111 TCTTC 720 AGCAG AGCAG 11111 |
| W22/1A B73/7-4 X112/8A X112/8A W22/1A | CACAA 11111 CACAA 11111 CACAA CTCGC 11111 CTCGC | CTACC 11111 CTACC 11111 CTACC 670 CTCCT CTCCT | TGGTC 11111 TGGTC 11111 TGGTC CTGGT CTGGT 11111 CTGGT | CTCGA CTCGA 11111 CTCGA 11111 CTCGA 680 CGACC 11111 CGACC | CGTCG 11111 CGTCG 11111 CGTCG GGGGC GGGGC 11111 aGGGCC | ACGAC 11111 ACGAC 11111 ACGAC 690 CGGTG 11111 CGGTG | ATCCC 11111 ATCCC 11111 ATCCC CTTGT 11111 CTTGT | CCGCG 11111 CCGCG 11111 CCGCG 700 CGACA CGACA 11111 CGACA | TCGTG 11111 TCGTG 11111 TCGTG TCCCC TCCCC 111111 TCCCC | CAGGA 11111 CAGGA 11111 CAGGA 710 AAGGA AAGGA 11111 | GGCTT 11111 GGCTT 11111 GGCTT CATCC 11111 CATCC | TCTTC 11111 TCTTC 11111 TCTTC 720 AGCAG AGCAG 11111 AGCAG |

| XI12/8A | CAGAT | 730 GGCGG | | 740 GTCTG | | | | | CTGGG | | TGCGC | 780 GCCTT |
|---------------------------------------|--|---|---|---|---|--|---|---|---|---|---|---|
| ALLET GIT | Ondin | 00000 | , , , | 0.0.0 | | | | , , , , , | | | | |
| H55\19 | | | | GTCTG | | | | | | | | |
| | | | | 11111 | | | | | | | | |
| B73/7-4 | | | | GTCTG | | | | | | | | |
| | | | | 11111 | | | | | | | | |
| XI12/8A | CAGAI | ննննն | IGCCI | GTCTG | GUACA | AULUU | ATUAU | ICIUC | ՄՈՍՍՍ | IACAI | Iblbl | UCCII |
| | | 790 | | 800 | | 810 | | 820 | | 830 | | 840 |
| XI12/8A | ΑΔΊΊ | | CTGCG | ACTGA | | | | | | | TGAAT | |
| ALIL/ OII | 000111 | 00000 | 01404 | no run | urrau | Trana | Uniqu'i | 00100 | 0.0 | 477.00 | | > |
| X22/1A | CCCAA | GCCCC | GTGCG | ACTGA | GTTGC | TTGAG | CAGGT | GCTGC | GTCTT | GTTGG | TGAAT | CCCGG |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
| B73/7-4 | | | | ACTGA | | | | | | | | _ |
| | | | | 11111 | | | | | | | | |
| XI15/84 | CCCAA | GCCCC | CTGCG | ACTGA | GTTGC | TTGAG | CAGGT | GCTGC | GTCTT | GTTGG | TGAAT | CCCGG |
| | | | | | | | | | | | | |
| | | QSN | | 86.0 | | 970 | | RRN | | ደዋበ | | 900 |
| Y112/9A | ıııı | | TTTAT | | | | | | GTGAG | | GCGAC | 900 GCTTT |
| A8/211X | CGCCC | | | 860 GTTGG > | | | | | | | GCGAC | |
| AB\S11X | | TGTTC | TTTAT | | CGGTG | CGTGC | GCAGC | ATCTG | GTGAG | GAGTT | | GCTTT |
| | CGCCC | TGTTC TGTTC | TITAT | GTTGG > | CGGTG CGGTG | CGTGC GCTGC | GCAGC GCAGC | ATCTG ATCTG | GTGAG GTGAG | GAGTT GAGTT | GCGAC | GCTTT GCTTT |
| | CGCCC 11111 CGCCC | TGTTC TGTTC LILL TGTTC | TTTAT TTTAT 11111 TTTAT | GTTGG > GTTGG 11 11 GTgGG | CGGTG CGGTG 11111 CGGTG | CGTGC GCTGC 11111 GCTGC | GCAGC GCAGC 11111 GCAGC | ATCTG ATCTG 11111 ATCTG | GTGAG GTGAG 11111 GTGAG | GAGTT GAGTT 11111 GAGTT | GCGAC 11111 GCGAC | GCTTT 11111 GCTTT |
| W22/1A B73/7-4 | CGCCC 11111 CGCCC 11111 | TGTTC TGTTC 11111 TGTTC 11111 | TTTAT TTTAT LITTAT TTTAT LITTAT LITTAT | GTTGG > GTTGG 11 11 GTgGG 11 11 | CGGTG 11111 CGGTG 11111 | CGTGC GCTGC 11111 GCTGC 11111 | GCAGC 11111 GCAGC 11111 | ATCTG 11111 ATCTG 11111 | GTGAG GTGAG 11111 GTGAG 11111 | GAGTT 11111 GAGTT 11111 | GCGAC 11111 GCGAC 11111 | GCTTT 11111 GCTTT 11111 |
| 422/1A | CGCCC 11111 CGCCC 11111 | TGTTC TGTTC 11111 TGTTC 11111 | TTTAT TTTAT LITTAT TTTAT LITTAT LITTAT | GTTGG > GTTGG 11 11 GTgGG | CGGTG 11111 CGGTG 11111 | CGTGC GCTGC 11111 GCTGC 11111 | GCAGC 11111 GCAGC 11111 | ATCTG 11111 ATCTG 11111 | GTGAG GTGAG 11111 GTGAG 11111 | GAGTT 11111 GAGTT 11111 | GCGAC 11111 GCGAC 11111 | GCTTT 11111 GCTTT 11111 |
| W22/1A B73/7-4 | CGCCC 11111 CGCCC 11111 | TGTTC 11111 TGTTC 11111 TGTTC 11111 TGTTC | TITAT TITAT 11111 TITAT 11111 TITAT | GTTGG CTTGG 11 11 GTgGG 11 11 GTTGG | CGGTG CGGTG 11111 CGGTG 11111 CGGTG | CGTGC GCTGC 11111 GCTGC 11111 GCTGC | GCAGC 11111 GCAGC 11111 GCAGC | ATCTG 11111 ATCTG 11111 ATCTG | GTGAG GTGAG 11111 GTGAG 11111 GTGAG | GAGTT 11111 GAGTT 11111 GAGTT GAGTT | GCGAC 11111 GCGAC 11111 GCGAC | GCTTT 11111 GCTTT 11111 GCTTT |
| W22/1A B73/7-4 XI12/8A | CGCCC 11111 CGCCC 11111 CGCCC | TGTTC 11111 TGTTC 11111 TGTTC 11111 TGTTC 910 | TTTAT TTTAT 11111 TTTAT 11111 TTTAT | GTTGG > GTTGG 11 11 GTgGG 11 11 GTTGG | CGGTG CGGTG 11111 CGGTG 11111 CGGTG | CGTGC GCTGC 11111 GCTGC 11111 GCTGC | GCAGC 11111 GCAGC 11111 GCAGC | ATCTG 11111 ATCTG 11111 ATCTG 940 | GTGAG GTGAG 11111 GTGAG 11111 GTGAG | GAGTT 11111 GAGTT 11111 GAGTT GAGTT 950 | GCGAC 11111 GCGAC 11111 GCGAC | GCTTT 11111 GCTTT 11111 GCTTT 11111 GCTTT 960 |
| W22/1A B73/7-4 | CGCCC 11111 CGCCC 11111 CGCCC | TGTTC 11111 TGTTC 11111 TGTTC 11111 TGTTC 910 | TTTAT TTTAT 11111 TTTAT 11111 TTTAT | GTTGG CTTGG 11 11 GTgGG 11 11 GTTGG | CGGTG CGGTG 11111 CGGTG 11111 CGGTG | CGTGC GCTGC 11111 GCTGC 11111 GCTGC | GCAGC 11111 GCAGC 11111 GCAGC | ATCTG 11111 ATCTG 11111 ATCTG 940 | GTGAG GTGAG 11111 GTGAG 11111 GTGAG | GAGTT 11111 GAGTT 11111 GAGTT GAGTT 950 | GCGAC 11111 GCGAC 11111 GCGAC | GCTTT 11111 GCTTT 11111 GCTTT 11111 GCTTT 960 |
| W22/1A B73/7-4 XI12/8A | CGCCC 11111 CGCCC 11111 CGCCC | TGTTC TGTTC 11111 TGTTC 11111 TGTTC 910 GCTGA | TTTAT TTTAT 11111 TTTAT 11111 TTTAT CTGGA | GTTGG > GTTGG 11 11 GTgGG 11 11 GTTGG | CGGTG CGGTG 11111 CGGTG 11111 CGGTG GGTCA | CGTGC GCTGC 11111 GCTGC 11111 GCTGC 930 CAACT | GCAGC 11111 GCAGC 11111 GCAGC ACTCT | ATCTG 11111 ATCTG 11111 ATCTG 4TCTG 940 TATGG | GTGAG GTGAG 11111 GTGAG 11111 GTGAG GCCTC | GAGTT 11111 GAGTT 11111 GAGTT 950 GGCAA | GCGAC 11111 GCGAC 11111 GCGAC | GCTTT 11111 GCTTT 11111 GCTTT 11111 GCTTT 960 CCAGC |
| W22/1A B73/7-4 XI12/8A XI12/8A | CGCCC 11111 CGCCC 11111 CGCCC | TGTTC TGTTC 11111 TGTTC 11111 TGTTC 910 GCTGA | TTTAT TTTAT 11111 TTTAT 11111 TTTAT CTGGA CTGGA | GTTGG CTTGG 11 11 GTgGG 11 11 GTTGG 920 ATCCC | CGGTG CGGTG 11111 CGGTG 11111 CGGTG GGTCA | CGTGC GCTGC 11111 GCTGC 11111 GCTGC 930 CAACT | GCAGC 11111 GCAGC 11111 GCAGC ACTCT | ATCTG 11111 ATCTG 11111 ATCTG 940 TATGG | GTGAG 11111 GTGAG 11111 GTGAG GCCTC | GAGTT 11111 GAGTT 11111 GAGTT 950 GGCAA | GCGAC 11111 GCGAC 11111 GCGAC CTTCC | GCTTT 11111 GCTTT 11111 GCTTT 960 CCAGC |
| W22/1A B73/7-4 XI12/8A XI12/8A | CGCCC 11111 CGCCC 11111 CGCCC GTGGA GTGGA 11111 GTGGA | TGTTC TGTTC 11111 TGTTC 11111 TGTTC 910 GCTGA 11111 GCTGA | TITAT TITAT 11111 TITAT 11111 TITAT CTGGA CTGGA 11111 CTGGA | GTTGG CTTGG 11 11 GTgGG 11 11 GTTGG 920 ATCCC ATCCC 11111 ATCCC | CGGTG 11111 CGGTG 11111 CGGTG GGTCA GGTCA 11111 GGTCA | CGTGC 11111 GCTGC 11111 GCTGC 930 CAACT 11111 CAACT | GCAGC 11111 GCAGC 11111 GCAGC ACTCT ACTCT 11111 ACTCT | ATCTG 11111 ATCTG 11111 ATCTG 940 TATGG 11111 TATGG | GTGAG 11111 GTGAG 11111 GTGAG GCCTC 11111 GCCTC | GAGTT 11111 GAGTT 11111 GAGTT 950 GGCAA 11111 GGCAA | GCGAC 11111 GCGAC 11111 GCGAC CTTCC 11111 CTTCC | GCTTT 11111 GCTTT 11111 GCTTT 960 CCAGC CCAGC 11111 CCAGC |
| W22/1A B73/7-4 X112/8A X112/8A W22/1A | CGCCC 11111 CGCCC 11111 CGCCC GTGGA GTGGA 11111 GTGGA 11111 | TGTTC 11111 TGTTC 11111 TGTTC 11111 TGTTC 910 GCTGA 11111 GCTGA 11111 | TITAT TITAT 11111 TITAT 11111 TITAT CTGGA CTGGA 11111 CTGGA 11111 | GTTGG CTTGG 11 11 GT9GG 11 11 GTTGG 920 ATCCC ATCCC 11111 | CGGTG 11111 CGGTG 11111 CGGTG GGTCA GGTCA 11111 GGTCA 11111 | CGTGC 11111 GCTGC 11111 GCTGC 930 CAACT CAACT 11111 CAACT 11111 | GCAGC 11111 GCAGC 11111 GCAGC ACTCT ACTCT 11111 ACTCT 11111 | ATCTG 11111 ATCTG 11111 ATCTG 940 TATGG 11111 TATGG 11111 | GTGAG GTGAG 11111 GTGAG 11111 GTGAG GCCTC GCCTC 11111 GCCTC 11111 | GAGTT 11111 GAGTT 11111 GAGTT 950 GGCAA 11111 GGCAA 11111 | GCGAC 11111 GCGAC 11111 GCGAC CTTCC CTTCC 11111 CTTCC 11111 | GCTTT 11111 GCTTT 11111 GCTTT 11111 GCTTT 960 CCAGC 11111 CCAGC 11111 |

| | | • • • | | | | | | | | | | |
|---------------------------------------|--|--|---|---|---|---|---|--|---|---|---|--|
| XI12/8A | GACGA | CCCAC | TGTCT | CTGCG | CATGC | TAGGT | ATGCA | TGGCA | CGGTG | TATGC | AAATT | ATGCA |
| H55\19 | | | TGTCT | | | | | | | | | |
| D70/7 A | | | 11111 | | | | | | | | | |
| B73/7-4 | | | TGTCT 11111 | | | | | | | | | |
| XI12/8A | | | TGTCT | | | | | | | | | |
| | | 1030 | | 1040 | | 1050 | | 1060 | | 1070 | | 1080 |
| XI12/8A | GTGGA | | CCGAT | | | | | | | | | , |
| H22/1A | GTGGA | TAAGG | CCGAT | CTGTT | GCTTG | CACTT | GGTGT | GCGGT | TTGAT | GATCG | TGTGA | CAGGG> |
| | | | 11111 | | | | | | | | | |
| B73/7-4 | | | | | | | | | | | | CAGGG> |
| W. A. O. /O. A | | | 11111 | | | | | | | | 1111 | |
| X112/8A | և I ևևA | IAAGU | CCGAT | CIGII | UCIIU | CACTI | սս I և I | նենն | HUAI | bAICU | 1616A | CAUUU |
| | | | | | | | | | | | | |
| | | 1090 | | 1100 | | 1110 | | 1120 | | 1130 | : | 1140 |
| X112/8A | AAGAT | | CTTTT | | | | | | | | | |
| XI12/8A | AAGAT | | стттт | | | | | | | | | |
| XI12/8A W22/1A | | TGAGG | | GCAAG | CAGGG | CTAAG | ATTGT | GCACG | TTGAT | ATTGA | TCCGG | CTGAG |
| | AAGAT | TGAGG TGAGG | CTTTT | GCAAG GCAAG | CAGGG CAGGG | CTAAG CTAAG | ATTGT ATTGT | GCACG GCACG | TTGAT TTGAT | ATTGA ATTGA | TCCGG TCCGG | CTGAG CTGAG |
| | AAGAT 11111 AAGAT | TGAGG TGAGG 11111 TGAGG | CTTTT CTTTT LLLLLL CTTTT | GCAAG 11111 GCAAG | CAGGG CAGGG 11111 CAGGG | CTAAG CTAAG 11111 CTAAG | ATTGT ATTGT 11111 ATTGT | GCACG GCACG 11111 GCACG | TTGAT TTGAT 11111 TTGAT | ATTGA ATTGA 11111 ATTGA | TCCGG 11111 TCCGG | CTGAG CTGAG 11111 CTGAG |
| W22/1A B73/7-4 | AAGAT 11111 AAGAT 11111 | TGAGG TGAGG 11111 TGAGG 11111 | CTTTT CTTTT 11111 CTTTT 11111 | GCAAG 11111 GCAAG 11111 | CAGGG 11111 CAGGG 11111 | CTAAG 11111 CTAAG 11111 | ATTGT 11111 ATTGT 11111 | GCACG GCACG 11111 GCACG 11111 | TTGAT TTGAT 11111 TTGAT 11111 | ATTGA ATTGA 11111 ATTGA 11111 | TCCGG 11111 TCCGG 11111 | CTGAG CTGAG 11111 CTGAG 11111 |
| H22/1A | AAGAT 11111 AAGAT 11111 | TGAGG TGAGG 11111 TGAGG 11111 | CTTTT CTTTT LLLLLL CTTTT | GCAAG 11111 GCAAG 11111 | CAGGG 11111 CAGGG 11111 | CTAAG 11111 CTAAG 11111 | ATTGT 11111 ATTGT 11111 | GCACG GCACG 11111 GCACG 11111 | TTGAT TTGAT 11111 TTGAT 11111 | ATTGA ATTGA 11111 ATTGA 11111 | TCCGG 11111 TCCGG 11111 | CTGAG CTGAG 11111 CTGAG 11111 |
| W22/1A B73/7-4 | AAGAT 11111 AAGAT 11111 | TGAGG TGAGG 11111 TGAGG 11111 TGAGG | CTTTT CTTTT 11111 CTTTT 11111 CTTTT | GCAAG 11111 GCAAG 11111 GCAAG | CAGGG 11111 CAGGG 11111 CAGGG | CTAAG 11111 CTAAG 11111 CTAAG | ATTGT 11111 ATTGT 11111 ATTGT ATTGT | GCACG 11111 GCACG 11111 GCACG | TTGAT TTGAT 11111 TTGAT 11111 TTGAT | ATTGA 11111 ATTGA 11111 ATTGA | TCCGG 11111 TCCGG 11111 TCCGG | CTGAG 11111 CTGAG 11111 CTGAG |
| W22/1A B73/7-4 XI12/BA | AAGAT 11111 AAGAT 11111 AAGAT | TGAGG TGAGG 11111 TGAGG 11111 TGAGG 11111 TGAGG | CTTTT 11111 CTTTT 11111 CTTTT CTTTT | GCAAG 11111 GCAAG 11111 GCAAG 1160 | CAGGG 11111 CAGGG 11111 CAGGG | CTAAG 11111 CTAAG 11111 CTAAG 1170 | ATTGT 11111 ATTGT 11111 ATTGT ATTGT | GCACG 11111 GCACG 11111 GCACG 1180 | TTGAT TTGAT 11111 TTGAT 11111 TTGAT | ATTGA 11111 ATTGA 11111 ATTGA 11111 ATTGA | TCCGG TCCGG 11111 TCCGG 11111 TCCGG | CTGAG CTGAG 11111 CTGAG 11111 CTGAG 1200 |
| W22/1A B73/7-4 | AAGAT 11111 AAGAT 11111 AAGAT | TGAGG TGAGG 11111 TGAGG 11111 TGAGG 11111 TGAGG | CTTTT 11111 CTTTT 11111 CTTTT CTTTT | GCAAG 11111 GCAAG 11111 GCAAG 1160 | CAGGG 11111 CAGGG 11111 CAGGG | CTAAG 11111 CTAAG 11111 CTAAG 1170 | ATTGT 11111 ATTGT 11111 ATTGT ATTGT | GCACG 11111 GCACG 11111 GCACG 1180 | TTGAT TTGAT 11111 TTGAT 11111 TTGAT | ATTGA 11111 ATTGA 11111 ATTGA 11111 ATTGA | TCCGG TCCGG 11111 TCCGG 11111 TCCGG | CTGAG CTGAG 11111 CTGAG 11111 CTGAG 1200 |
| W22/1A B73/7-4 XI12/BA | AAGAT 11111 AAGAT 11111 AAGAT ATTGG | TGAGG 11111 TGAGG 11111 TGAGG 1150 CAAGA | CTTTT 11111 CTTTT 11111 CTTTT ACAAG | GCAAG 11111 GCAAG 11111 GCAAG 11160 CAGCC CAGCC | CAGGG 11111 CAGGG 11111 CAGGG ACATG | CTAAG 11111 CTAAG 11111 CTAAG 1170 TGTCC TGTCC | ATTGT 11111 ATTGT 11111 ATTGT ATCTG ATCTG | GCACG 11111 GCACG 11111 GCACG 1180 TGCAG | TTGAT TTGAT TTGAT TTGAT TTGAT TTGAT ATGTT | ATTGA 11111 ATTGA 11111 ATTGA 1190 AAGCT | TCCGG 11111 TCCGG 11111 TCCGG 11111 TCCGG TGCTT | CTGAG CTGAG 11111 CTGAG 11111 CTGAG 1200 TGCAG TGCAG |
| W22/1A B73/7-4 XI12/8A XI12/8A W22/1A | AAGAT 11111 AAGAT 11111 AAGAT ATTGG 11111 | TGAGG TGAGG 11111 TGAGG 11111 TGAGG 1150 CAAGA 11111 | CTTTT 11111 CTTTT 11111 CTTTT ACAAG ACAAG 11111 | GCAAG 11111 GCAAG 11111 GCAAG 1160 CAGCC CAGCC 11111 | CAGGG 11111 CAGGG 11111 CAGGG ACATG ACATG | CTAAG 11111 CTAAG 11111 CTAAG 1170 TGTCC TGTCC 11111 | ATTGT 11111 ATTGT 11111 ATTGT ATCTG ATCTG 11111 | GCACG GCACG 11111 GCACG 11111 GCACG TGCAG 11111 | TTGAT TTGAT 11111 TTGAT 11111 TTGAT ATGTT ATGTT 11111 | ATTGA ATTGA 11111 ATTGA 11111 ATTGA 1190 AAGCT AAGCT 11111 | TCCGG TCCGG 11111 TCCGG 11111 TCCGG TGCTT TGCTT 11111 | CTGAG CTGAG 11111 CTGAG 11111 CTGAG 1200 TGCAG TGCAG 11111 |
| W22/1A B73/7-4 XI12/8A XI12/8A | AAGAT 11111 AAGAT 11111 AAGAT ATTGG 11111 ATTGG | TGAGG 11111 TGAGG 11111 TGAGG 1150 CAAGA CAAGA | CTTTT 11111 CTTTT 11111 CTTTT ACAAG ACAAG 11111 ACAAG | GCAAG 11111 GCAAG 11111 GCAAG 1160 CAGCC 11111 CAGCC | CAGGG 11111 CAGGG 11111 CAGGG ACATG ACATG 11111 ACATG | CTAAG 11111 CTAAG 11111 CTAAG 1170 TGTCC 11111 TGTCC | ATTGT 11111 ATTGT 11111 ATTGT ATCTG 11111 ATCTG 11111 ATCTG | GCACG 11111 GCACG 11111 GCACG 1180 TGCAG 11111 TGCAG | TTGAT TTGAT TTGAT TTGAT TTGAT TTGAT TTGAT TTGAT ATGTT ATGTT ATGTT ATGTT | ATTGA 11111 ATTGA 11111 ATTGA 1190 AAGCT 11111 AAGCT | TCCGG 11111 TCCGG 11111 TCCGG 11111 TCCGG TGCTT 11111 TGCTT | CTGAG CTGAG 11111 CTGAG 11111 CTGAG 1200 TGCAG TGCAG 11111 TGCAG |
| W22/1A B73/7-4 XI12/8A XI12/8A W22/1A | AAGAT 11111 AAGAT 11111 AAGAT ATTGG 11111 ATTGG 11111 | TGAGG TGAGG TITT TGAGG TTT TTT | CTTTT 11111 CTTTT 11111 CTTTT ACAAG ACAAG 11111 | GCAAG 11111 GCAAG 11111 GCAAG 11160 CAGCC CAGCC 11111 CAGCC 11111 | CAGGG 11111 CAGGG 11111 CAGGG ACATG ACATG ACATG 11111 ACATG 11111 | CTAAG 11111 CTAAG 11111 CTAAG 11170 TGTCC TGTCC 11111 TGTCC 11111 | ATTGT 11111 ATTGT 11111 ATTGT ATCTG ATCTG 11111 ATCTG 11111 | GCACG 11111 GCACG 11111 GCACG 1180 TGCAG TGCAG 11111 TGCAG 11111 | TTGAT TTGAT 11111 TTGAT 11111 TTGAT ATGTT ATGTT 11111 ATGTT 11111 | ATTGA 11111 ATTGA 11111 ATTGA 1190 AAGCT AAGCT 11111 AGCT 11111 | TCCGG 11111 TCCGG 11111 TCCGG 11111 TCCGG TGCTT TGCTT 11111 TGCTT 11111 | CTGAG CTGAG 11111 CTGAG 11111 CTGAG 1200 TGCAG TGCAG 11111 TGCAG 11111 |

| | | 1210 | | 1220 | | 1230 | | 1240 | | 1250 | | 1260 |
|---|---|--|---|--|---|--|---|--|---|--|---|--|
| XI12/8A | GGCAT | GAATG | CTCTT | CTTGA | AGGAA | GCACA | TCAAA | GAAGA | GCTTT | GACTT | TGGCT | CATGG |
| M22/1A | GGCAT | GAATG | CTCTT | CTTGA | AGGAA | GCACA | TCAAA | GAAGA | GCTTT | GACTT | TGGCT | CATGG |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
| B73/7-4 | GGCAT | GAATG | CTCTT | CTTGA | aggaa | GCACA | TCAAA | GAAGA | GCTTT | GACTT | TGGCT | CATGG |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
| XI12/8A | GGCAT | GAATG | CTCTT | CTTGA | AGGAA | GCACA | TCAAA | GAAGA | GCTTT | GACTT | TGGCT | CATGG |
| | | 1270 | | 1280 | | 1290 | | 1300 | | 1310 | • | 1320 |
| X112/8A | ΔΔΓΓΙΔ | | ΤΓΓΕΔΤ | | GAAGA | | | | GGTAT | AAAAC | ΔΤΩΤΔ | |
| ATTE/ UN | nnoun | TUNUT | Tuoni | UNUUN | Unnun | uuunn | 11000 | CCTTU | uuini | nnnnu | псп | munu |
| H22/1A | AACGA | TGAGT | TGGAT | CAGCA | GAAGA | GGGAA | TTCCC | CCTTG | GGTAT | AAAAC | ATCTA | ATGAG |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
| B73/65 | AACGA | TGAGT | TGGAT | CAGCA | GAAGA | GGGAA | TTCCC | CCTTG | GGTAT | AAAAC | ATCTA | ATGAG |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
| XI12/8A | AACGA | TGAGT | TGGAT | CAGCA | GAAGA | GGGAA | TTCCC | CCTTG | GGTAT | AAAAC | ATCTA | ATGAG |
| | | | | | | | | | | | | |
| | | 1330 | | 1340 | | 1350 | | 1360 | | 1370 | | 1380 |
| A8/211X | GAGAT | 1330 CCAGC | AAAA | 1340 TATGC | TATTC | | CTTGA | | TGACG | 1370 AAAGG | CEAGG | 1380 CCATC |
| XI12/8A | GAGAT | | CACAA | | TATTC | | | | TGACG | 1370 AAAGG | CGAGG | |
| XI12/8A W22/1A | | CCAGC | | TATGC | | AGGTT | CTTGA | TGAGC | | | | CCATC |
| | GAGAT | CCAGC CCAGC | CACAA | TATGC TATGC | TATTC | AGGTT AGGTT | CTTGA CTTGA | TGAGC TGAGC | TGACG | AAAGG | CGAGG | CCATC CCATC |
| | GAGAT 11111 GAGAT | CCAGC CCAGC 11111 CCAGC | CACAA 11111 CACAA | TATGC TATGC 11111 TATGC | TATTC 11111 TATTC | AGGTT AGGTT 11111 AGGTT | CTTGA CTTGA 11111 CTTGA | TGAGC TGAGC 11111 TGAGC | TGACG 11111 TGACG | AAAGG 11111 AAAGG | CGAGG 11111 CGAGG | CCATC CCATC 11111 CCATC |
| H22/1A | GAGAT 11111 GAGAT 11111 | CCAGC 11111 CCAGC 11111 | CACAA 11111 CACAA 11111 | TATGC TATGC 11111 TATGC 11111 | TATTC 11111 TATTC 11111 | AGGTT 11111 AGGTT 11111 | CTTGA CTTGA 11111 CTTGA 11111 | TGAGC 11111 TGAGC 11111 | TGACG 11111 TGACG 11111 | AAAGG 11111 AAAGG 11111 | CGAGG 11111 CGAGG 11111 | CCATC 11111 CCATC 11111 |
| H22/1A | GAGAT 11111 GAGAT 11111 | CCAGC 11111 CCAGC 11111 | CACAA 11111 CACAA 11111 | TATGC TATGC 11111 TATGC 11111 | TATTC 11111 TATTC 11111 | AGGTT 11111 AGGTT 11111 | CTTGA CTTGA 11111 CTTGA 11111 | TGAGC 11111 TGAGC 11111 | TGACG 11111 TGACG 11111 | AAAGG 11111 AAAGG | CGAGG 11111 CGAGG 11111 | CCATC 11111 CCATC 11111 |
| H22/1A B73/7-4 | GAGAT 11111 GAGAT 11111 | CCAGC 11111 CCAGC 11111 CCAGC | CACAA 11111 CACAA 11111 | TATGC TATGC 11111 TATGC 11111 TATGC | TATTC 11111 TATTC 11111 | AGGTT 11111 AGGTT 11111 AGGTT AGGTT AGGTT | CTTGA CTTGA 11111 CTTGA 11111 CTTGA | TGAGC 11111 TGAGC 11111 TGAGC | TGACG 11111 TGACG 11111 | AAAGG 11111 AAAGG 11111 AAAGG | CGAGG 11111 CGAGG 11111 | CCATC CCATC 111111 CCATC 111111 CCATC |
| H22/1A B73/7-4 XI12/8A | GAGAT 11111 GAGAT 11111 GAGAT | CCAGC 11111 CCAGC 11111 CCAGC 11111 CCAGC | CACAA 11111 CACAA 11111 CACAA | TATGC TATGC 11111 TATGC 11111 TATGC 1400 | TATTC 11111 TATTC 11111 TATTC | AGGTT 11111 AGGTT 11111 AGGTT 1410 | CTTGA CTTGA 11111 CTTGA 11111 CTTGA | TGAGC TGAGC 11111 TGAGC 11111 TGAGC | TGACG 11111 TGACG 11111 TGACG | AAAGG 11111 AAAGG 11111 AAAGG 1430 | CGAGG 11111 CGAGG 11111 CGAGG | CCATC 11111 CCATC 11111 CCATC 11111 CCATC 1440 |
| H22/1A B73/7-4 | GAGAT 11111 GAGAT 11111 GAGAT | CCAGC 11111 CCAGC 11111 CCAGC 11111 CCAGC | CACAA 11111 CACAA 11111 CACAA | TATGC TATGC 11111 TATGC 11111 TATGC 1400 | TATTC 11111 TATTC 11111 TATTC | AGGTT 11111 AGGTT 11111 AGGTT 1410 | CTTGA CTTGA 11111 CTTGA 11111 CTTGA | TGAGC TGAGC 11111 TGAGC 11111 TGAGC | TGACG 11111 TGACG 11111 TGACG | AAAGG 11111 AAAGG 11111 AAAGG | CGAGG 11111 CGAGG 11111 CGAGG | CCATC 11111 CCATC 11111 CCATC 11111 CCATC 1440 |
| H22/1A B73/7-4 XI12/8A | GAGAT 11111 GAGAT 11111 GAGAT | CCAGC 11111 CCAGC 11111 CCAGC 1390 CACAG | CACAA 11111 CACAA 11111 CACAA | TATGC TATGC 11111 TATGC 11111 TATGC 1400 GGGCA | TATTC 11111 TATTC 11111 TATTC | AGGTT 11111 AGGTT 11111 AGGTT 1410 AGATG | CTTGA CTTGA 11111 CTTGA 11111 CTTGA TGGGC | TGAGC TGAGC 11111 TGAGC 11111 TGAGC 1420 GGCAC | TGACG 11111 TGACG 11111 TGACG | AAAGG 11111 AAAGG 11111 AAAGG 1430 | CGAGG 11111 CGAGG 11111 CGAGG | CCATC 11111 CCATC 11111 CCATC 11111 CCATC 1440 AGCGG |
| H22/1A B73/7-4 XI12/8A XI12/8A | GAGAT 11111 GAGAT 11111 GAGAT ATCGG ATCGG 11111 | CCAGC 11111 CCAGC 11111 CCAGC 11111 CCAGC 1390 CACAG CACAG 11111 | CACAA 11111 CACAA 11111 CACAA GTGTT GTGTT 11111 | TATGC TATGC 11111 TATGC 11111 TATGC 1400 GGGCA GGGCA 11111 | TATTC 11111 TATTC 11111 TATTC GCACC GCACC 11111 | AGGTT 11111 AGGTT 11111 AGGTT 1410 AGATG 11111 | CTTGA CTTGA 11111 CTTGA 11111 CTTGA TGGGC TGGGC 11111 | TGAGC 11111 TGAGC 11111 TGAGC 1420 GGCAC GGCAC 11111 | TGACG 11111 TGACG 11111 TGACG AGTAC AGTAC 11111 | AAAGG 11111 AAAGG 11111 AAAGG 1430 TACAC TACAC 11111 | CGAGG 11111 CGAGG 11111 CGAGG TTACA TTACA | CCATC 11111 CCATC 11111 CCATC 11440 AGCGG AGCGG 11111 |
| H22/1A B73/7-4 XI12/8A XI12/8A | GAGAT 11111 GAGAT 11111 GAGAT ATCGG ATCGG 11111 | CCAGC 11111 CCAGC 11111 CCAGC 11111 CCAGC 1390 CACAG CACAG 11111 | CACAA 11111 CACAA 11111 CACAA GTGTT GTGTT 11111 | TATGC TATGC 11111 TATGC 11111 TATGC 1400 GGGCA GGGCA 11111 | TATTC 11111 TATTC 11111 TATTC GCACC GCACC 11111 | AGGTT 11111 AGGTT 11111 AGGTT 1410 AGATG 11111 | CTTGA CTTGA 11111 CTTGA 11111 CTTGA TGGGC TGGGC 11111 | TGAGC 11111 TGAGC 11111 TGAGC 1420 GGCAC GGCAC 11111 | TGACG 11111 TGACG 11111 TGACG AGTAC AGTAC 11111 | AAAGG 11111 AAAGG 11111 AAAGG 11111 AAAGG 1430 TACAC | CGAGG 11111 CGAGG 11111 CGAGG TTACA TTACA | CCATC 11111 CCATC 11111 CCATC 11440 AGCGG AGCGG 11111 |
| H22/1A B73/7-4 XI12/8A XI12/8A H22/1A | GAGAT 11111 GAGAT 11111 GAGAT ATCGG ATCGG 11111 ATCGG | CCAGC 11111 CCAGC 11111 CCAGC 1390 CACAG CACAG 11111 CACAG | CACAA 11111 CACAA 11111 CACAA GTGTT GTGTT 11111 GTGTT | TATGC TATGC 11111 TATGC 11111 TATGC 1400 GGGCA GGGCA 11111 GGGCA | TATTC 11111 TATTC 11111 TATTC GCACC GCACC 11111 GCACC | AGGTT 11111 AGGTT 11111 AGGTT 1410 AGATG 11111 AGATG | CTTGA CTTGA 11111 CTTGA 11111 CTTGA TGGGC TGGGC 11111 TGGGC | TGAGC 11111 TGAGC 11111 TGAGC 1420 GGCAC 11111 GGCAC | TGACG 11111 TGACG 11111 TGACG AGTAC AGTAC 11111 AGTAC | AAAGG 11111 AAAGG 11111 AAAGG 1430 TACAC TACAC 11111 | CGAGG 11111 CGAGG 11111 CGAGG TTACA TTACA 11111 TTACA | CCATC 11111 CCATC 11111 CCATC 1440 AGCGG 11111 AGCGG |
| #22/1A B73/7-4 XI12/8A XI12/8A #22/1A | GAGAT 11111 GAGAT 11111 GAGAT ATCGG 11111 ATCGG 11111 | CCAGC 11111 CCAGC 11111 CCAGC 1390 CACAG CACAG 11111 CACAG 11111 | CACAA 11111 CACAA 11111 CACAA GTGTT GTGTT 11111 GTGTT 11111 | TATGC TATGC 11111 TATGC 11111 TATGC 1400 GGGCA GGGCA 11111 GGGCA 11111 | TATTC 11111 TATTC 11111 TATTC GCACC IIIII GCACC IIIII | AGGTT 11111 AGGTT 11111 AGGTT 1410 AGATG 11111 AGATG 11111 | CTTGA 11111 CTTGA 11111 CTTGA 11111 CTTGA TGGGC 11111 TGGGC 11111 | TGAGC 11111 TGAGC 11111 TGAGC 11111 TGAGC 1420 GGCAC 11111 GGCAC 11111 | TGACG 11111 TGACG 11111 TGACG AGTAC AGTAC 11111 AGTAC 11111 | AAAGG 11111 AAAGG 11111 AAAGG 11111 AAAAGG TACAC TACAC 11111 TACAC | CGAGG 11111 CGAGG 11111 CGAGG TTACA TTACA 11111 TTACA 11111 | CCATC 11111 CCATC 11111 CCATC 1440 AGCGG 11111 AGCGG 11111 |

| | | 1450 | | 1460 | | 1470 | | 1480 | | 1490 | | 1500 |
|---------------------------------------|--|--|---|--|---|--|---|---|---|--|--|--|
| X112/8A | CCAAG | GCAGT | GGTTG | TCTTC | AGCTG | GTCTT | GGGGC | TATGG | GATTT | GGTTT | GCCGG | CTGCT |
| A1/25B | CCAAG | GCAGT | GGTTG | TCTTC | AGCTG | GTCTT | GGGGC | TATGG | GATTT | GGTTT | GCCGG | CTGCT |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
| B73/7-4 | CCAAG | GCAGT | GGTTG | TCTTC | AGCTG | GTCTT | GGGGC | TATGG | GATTT | GGTTT | GCCGG | CTGCT |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
| X112/8A | CCAAG | GCAGT | GGTTG | TCTTC | AGCTG | GTCTT | GGGGC | TATGG | GATTT | GGTTT | GCCGG | CTGCT |
| | | 1510 | ÷ | 1520 | | 1530 | | 1540 | | 1550 | | 1560 |
| XI12/8A | GCTGG | | CTGTG | | | | | | | | | |
| | | | | | | > | | | | | | |
| H22/1A | | | CTGTG | | | | | | | | | |
| | | | 11111 | | | | | | | | 11111 | |
| B73/7-4 | | | CTGTG | | | | | | | | | |
| | | | 11111 | | | | | | | | | |
| XI12/8A | GCTGG | TGCTT | CTGTG | GCCAA | CCCAG | GTGTT | ACTGT | 16116 | ACATC | GATGG | AGATG | GTAGC |
| | | | | | | | | | | | | |
| | | 1570 | | 1580 | | 1590 | | 1600 | | 1610 | | 1620 |
| AR/CITY | TTTCT | 1570 CATGA | | | | | ATCCG | | | | | 1620 AGGTC |
| XI12/8A | TITCT | | ACGTT | | | | | | | | | |
| XI12/8A U22/1A | | CATGA | | CAGGA | GCTAG | CTATG | ATCCG | AATTG | AGAAC | CTCCC | GGTGA > | AGGTC |
| | TTTCT 11111 | CATGA CATGA 11111 | ACGTT ACGTT 11111 | CAGGA CAGGA 11111 | GCTAG GCTAG 11111 | CTATG CTATG 11111 | ATCCG 11111 | AATTG 11111 | AGAAC 11111 | CTCCC CTCCC 11111 | GGTGA > GGTGA 1111 | AGGTC 11111 |
| | TTTCT L1111 TTTCT | CATGA CATGA 11111 CATGA | ACGTT ACGTT 11111 ACGTT | CAGGA CAGGA 11111 CAGGA | GCTAG GCTAG 11111 GCTAG | CTATG CTATG 11111 CTATG | ATCCG 11111 ATCCG | AATTG 11111 AATTG | AGAAC 11111 AGAAC | CTCCC 11111 CTCCC | GGTGA GGTGA 1111 aGTGA | AGGTC 11111 AGGTC |
| H22/1A | TTTCT 11111 TTTCT 11111 | CATGA CATGA 11111 CATGA 11111 | ACGTT 11111 ACGTT 11111 | CAGGA 11111 CAGGA 11111 | GCTAG 11111 GCTAG 11111 | CTATG LILL CTATG LILL LILL | ATCCG 11111 ATCCG 11111 | AATTG 11111 AATTG 11111 | AGAAC 11111 AGAAC 11111 | CTCCC 11111 CTCCC 11111 | GGTGA GGTGA 1111 aGTGA 1111 | AGGTC 11111 AGGTC 11111 |
| H22/1A | TTTCT 11111 TTTCT 11111 | CATGA CATGA 11111 CATGA 11111 | ACGTT ACGTT 11111 ACGTT | CAGGA 11111 CAGGA 11111 | GCTAG 11111 GCTAG 11111 | CTATG LILL CTATG LILL LILL | ATCCG 11111 ATCCG 11111 | AATTG 11111 AATTG 11111 | AGAAC 11111 AGAAC 11111 | CTCCC 11111 CTCCC 11111 | GGTGA GGTGA 1111 aGTGA 1111 | AGGTC 11111 AGGTC 11111 |
| W22/1A B73/7-4 | TTTCT 11111 TTTCT 11111 | CATGA CATGA 11111 CATGA 11111 CATGA | ACGTT 11111 ACGTT 11111 ACGTT ACGTT | CAGGA 11111 CAGGA 11111 CAGGA | GCTAG GCTAG 11111 GCTAG 11111 GCTAG | CTATG 11111 CTATG 11111 CTATG CTATG | ATCCG 11111 ATCCG 11111 ATCCG | AATTG 11111 AATTG 11111 AATTG | AGAAC 11111 AGAAC 11111 AGAAC | CTCCC 11111 CTCCC 11111 CTCCC | GGTGA CGTGA 1111 CGTGA 1111 GGTGA | AGGTC 11111 AGGTC 11111 |
| W22/1A B73/7-4 | TTTCT 11111 TTTCT 11111 TTTCT | CATGA CATGA 11111 CATGA 11111 CATGA 11111 CATGA 1630 | ACGTT 11111 ACGTT 11111 ACGTT ACGTT | CAGGA CAGGA 11111 CAGGA 11111 CAGGA 1640 | GCTAG GCTAG 11111 GCTAG 11111 GCTAG | CTATG 11111 CTATG 11111 CTATG 11111 CTATG 1650 | ATCCG 11111 ATCCG 11111 ATCCG | AATTG 11111 AATTG 11111 AATTG 11111 AATTG | AGAAC 11111 AGAAC 11111 AGAAC | CTCCC 11111 CTCCC 11111 CTCCC 1670 | GGTGA CGTGA 1111 CGTGA 1111 GGTGA | AGGTC 11111 AGGTC 11111 AGGTC 11111 AGGTC 1680 |
| H22/1A B73/7-4 XI12/8A XI12/8A | TTTCT 11111 TTTCT 11111 TTTCT | CATGA CATGA 11111 CATGA 11111 CATGA 11630 GCTAA | ACGTT 11111 ACGTT 11111 ACGTT ACGTT ACAAC | CAGGA CAGGA 11111 CAGGA 11111 CAGGA 1640 CAGCA | GCTAG GCTAG 11111 GCTAG 11111 GCTAG CCTAG | CTATG 11111 CTATG 11111 CTATG 11111 CTATG 1650 GGATG | ATCCG 11111 ATCCG 11111 ATCCG GTGGT | AATTG 11111 AATTG 11111 AATTG 1660 GCAGT | AGAAC 11111 AGAAC 11111 AGAAC GGGAG | CTCCC 11111 CTCCC 11111 CTCCC 1670 GACAG | GGTGA CGTGA 1111 CGTGA 1111 GGTGA GTTCT | AGGTC 11111 AGGTC 11111 AGGTC 1680 ATAAG |
| W22/1A B73/7-4 XI12/8A | TTTCT 11111 TTTCT 11111 TTTCT TTTGT | CATGA CATGA 11111 CATGA 11111 CATGA 1630 GCTAA | ACGTT 11111 ACGTT 11111 ACGTT ACAAC ACAAC | CAGGA 11111 CAGGA 11111 CAGGA 1640 CAGCA | GCTAG 11111 GCTAG 11111 GCTAG CCTGG | CTATG 11111 CTATG 11111 CTATG 1650 GGATG | ATCCG 11111 ATCCG 11111 ATCCG GTGGT | AATTG 11111 AATTG 11111 AATTG 1660 GCAGT | AGAAC 11111 AGAAC 11111 AGAAC GGGAG | CTCCC 11111 CTCCC 11111 CTCCC 1670 GACAG | GGTGA CGTGA 1111 CGTGA 1111 GGTGA GTTCT | AGGTC 11111 AGGTC 11111 AGGTC 11111 AGGTC 1680 ATAAG |
| W22/1A B73/7-4 X112/8A X112/8A W22/1A | TTTCT 11111 TTTCT 11111 TTTCT TTTGT 11111 | CATGA CATGA 11111 CATGA 11111 CATGA 1630 GCTAA GCTAA 11111 | ACGTT 11111 ACGTT 11111 ACGTT ACAAC ACAAC 11111 | CAGGA CAGGA 11111 CAGGA 11111 CAGGA 1640 CAGCA CAGCA 11111 | GCTAG 11111 GCTAG 11111 GCTAG CCTGG CCTGG 11111 | CTATG 11111 CTATG 11111 CTATG 1650 GGATG 11111 | ATCCG 11111 ATCCG 111111 ATCCG GTGGT GTGGT 11111 | AATTG 11111 AATTG 11111 AATTG 1660 GCAGT GCAGT 11111 | AGAAC 11111 AGAAC 11111 AGAAC GGGAG GGGAG 11111 | CTCCC CTCCC 111111 CTCCC 111111 CTCCC 1670 GACAG GACAG 11111 | GGTGA CGTGA 1111 CGTGA GTTCT GTTCT 11111 | AGGTC 11111 AGGTC 11111 AGGTC 11111 AGGTC 1680 ATAAG ATAAG 11111 |
| H22/1A B73/7-4 XI12/8A XI12/8A | TTTCT 11111 TTTCT 11111 TTTCT TTTGT 11111 TTTGT 11111 TTTGT | CATGA CATGA 11111 CATGA 11111 CATGA 1630 GCTAA GCTAA 11111 GCTAA | ACGTT 11111 ACGTT 11111 ACGTT ACAAC ACAAC 111111 ACAAC | CAGGA 11111 CAGGA 11111 CAGGA 1640 CAGCA CAGCA 11111 CAGCA | GCTAG 11111 GCTAG 11111 GCTAG CCTGG 11111 CCTGG | CTATG 11111 CTATG 11111 CTATG 1650 GGATG 11111 GGATG | ATCCG 11111 ATCCG 11111 ATCCG GTGGT 11111 GTGGT | AATTG 11111 AATTG 11111 AATTG 1660 GCAGT 11111 GCAGT | AGAAC 11111 AGAAC 11111 AGAAC GGGAG 11111 GGGAG | CTCCC 11111 CTCCC 11111 CTCCC 1670 GACAG 11111 GACAG | GGTGA CGTGA 1111 CGTGA 1111 GGTGA GTTCT 11111 GTTCT 11111 | AGGTC 11111 AGGTC 11111 AGGTC 1680 ATAAG ATAAG 11111 ATAAG |
| W22/1A B73/7-4 X112/8A X112/8A W22/1A | TTTCT 11111 TTTCT 11111 TTTCT TTTGT 11111 TTTGT 11111 TTTGT 11111 | CATGA CATGA 11111 CATGA 11111 CATGA 1630 GCTAA GCTAA 11111 GCTAA 11111 | ACGTT 11111 ACGTT 11111 ACGTT ACAAC ACAAC 11111 ACAAC 11111 | CAGGA 11111 CAGGA 11111 CAGGA 1640 CAGCA CAGCA 11111 CAGCA 11111 | GCTAG 11111 GCTAG 11111 GCTAG CCTGG CCTGG 11111 CCTGG 11111 | CTATG 11111 CTATG 11111 CTATG 1650 GGATG 11111 GGATG 11111 | ATCCG 11111 ATCCG 11111 ATCCG GTGGT GTGGT 11111 GTGGT 11111 | AATTG 11111 AATTG 111111 AATTG 1660 GCAGT 11111 GCAGT 11111 | AGAAC 11111 AGAAC 11111 AGAAC GGGAG GGGAG 11111 GGGAG 11111 | CTCCC 11111 CTCCC 111111 CTCCC 1670 GACAG 11111 GACAG 11111 | GGTGA CGTGA 1111 CGTGA 1111 GGTGA GTTCT 11111 GTTCT 11111 GTTCT 11111 | AGGTC 11111 AGGTC 11111 AGGTC 1680 ATAAG ATAAG 11111 ATAAG |

| | 555.4 | 1690 | | | | | | 1720 | | | | 1740 |
|---------------------------------------|---|--|---|---|--|--|---|--|---|--|---|---|
| XI12/8A | GCCAA | CAGAG | CGCAC | ACATA | CIIGG | GAAAC | CCAGA | GAATG | AAAU1 | LALA I | AIAIC | CAGAI |
| A55\IV | - | | | | | | | GAATG | | | | |
| D70 <i>17_4</i> | | | | | | | | 11111 GAATG | | | | |
| B73/7-4 | | | | | | | | 11111 | | | | |
| XI12/8A | | | | | | | | GAATG | | | | |
| | | 1750 | | 1760 | | 1770 | | 1780 | | 1790 | | 1800 |
| XI12/8A | TTCGT | GACGA | TCGCC | AAAGG | GTTCA | ACATT | CCAGC | GGTCC | GTGTG | ACAAA | GAAGA | ACGAA |
| H22/1A | | | | | | | | GGTCC | | | | |
| | | | | | | | | 11111 | | | | |
| B73/7-4 | | | | | | | | GGTCC | | | | |
| W. 1.0. /O. | | | | | | | | 11111 | | | | |
| XI12/8A | 11661 | UALUA | ILULL | AAAbu | UIILA | ALAII | LLAUL | GGTCC | บเบเบ | ALAAA | UAAUA | ALUAA |
| | | | | | | | | | | | | |
| | | 1810 | | 1820 | | 1830 | | 1840 | | 1850 | | 1860 |
| X112/8A | GTCCG | 1810 CGCAG | | 0581 Aagaa | | | | 1840 AGGGC | | | GGATA | 1860 Taatc |
| | | CGCAG | CGATA | AAGAA | GATGC | TCGAG | ACTCC | AGGGC | CGTAC | CTCTT | | TAATC |
| X112/8A U22/1A | GTCCG | CGCAG CGCAG | CGATA CGATA | AAGAA | GATGC GATGC | TCGAG TCGAG | ACTCC ACTCC | AGGGC AGGGC | CGTAC CGTAC | CTCTT | GGATA | TAATC TAATC |
| H22/1A | GTCCG 11111 | CGCAG 11111 | CGATA CGATA 11111 | AAGAA 11111 | GATGC GATGC 11111 | TCGAG TCGAG 11111 | ACTCC ACTCC 11111 | AGGGC AGGGC 11111 | CGTAC 11111 | CTCTT CTCTT 11111 | GGATA 1111 | TAATC 11111 |
| | GTCCG 11111 GTCCG | CGCAG CGCAG 11111 CGCAG | CGATA CGATA 11111 CGATA | AAGAA 11111 AAGAA | GATGC GATGC 11111 GATGC | TCGAG TCGAG 11111 TCGAG | ACTCC ACTCC 11111 ACTCC | AGGGC AGGGC 11111 AGGGC | CGTAC 11111 CGTAC | CTCTT CTCTT 11111 CTCTT | GGATA 11111 GGATA | TAATC 11111 TAATC |
| H22/1A | GTCCG 11111 GTCCG 11111 | CGCAG 11111 CGCAG 11111 | CGATA 11111 CGATA 11111 | AAGAA 11111 AAGAA 11111 | GATGC 11111 GATGC 11111 | TCGAG TCGAG 11111 TCGAG 11111 | ACTCC 11111 ACTCC 11111 | AGGGC AGGGC 11111 | CGTAC 11111 CGTAC 11111 | CTCTT 11111 CTCTT 11111 | GGATA 11111 GGATA 11111 | TAATC 11111 TAATC 11111 |
| U22/1A B73/7-4 | GTCCG 11111 GTCCG 11111 | CGCAG 11111 CGCAG 11111 CGCAG | CGATA CGATA 11111 CGATA 11111 CGATA | AAGAA 11111 AAGAA 11111 AAGAA | GATGC GATGC 11111 GATGC 11111 GATGC | TCGAG TCGAG 11111 TCGAG 11111 TCGAG | ACTCC 11111 ACTCC 11111 ACTCC | AGGGC 11111 AGGGC 11111 AGGGC | CGTAC 11111 CGTAC 11111 CGTAC | CTCTT CTCTT 11111 CTCTT 11111 CTCTT | GGATA 11111 GGATA 11111 GGATA | TAATC 11111 TAATC 11111 TAATC |
| U22/1A B73/7-4 | GTCCG 11111 GTCCG 11111 GTCCG | CGCAG 11111 CGCAG 11111 CGCAG 11111 CGCAG 1870 | CGATA 11111 CGATA 11111 CGATA 11111 CGATA | AAGAA 11111 AAGAA 11111 AAGAA 1880 | GATGC GATGC 11111 GATGC 11111 GATGC | TCGAG 11111 TCGAG 11111 TCGAG 1890 | ACTCC 11111 ACTCC 11111 ACTCC | AGGGC 11111 AGGGC 11111 | CGTAC 11111 CGTAC 11111 CGTAC | CTCTT 11111 CTCTT 11111 CTCTT 11111 CTCTT 1910 | GGATA 11111 GGATA 11111 GGATA | TAATC 11111 TAATC 11111 TAATC 11111 TAATC 1920 |
| H22/1A B73/7-4 XI12/8A XI12/8A | GTCCG 11111 GTCCG 11111 GTCCG | CGCAG CGCAG 11111 CGCAG 11111 CGCAG 1870 ACACC | CGATA 11111 CGATA 11111 CGATA 11111 CGATA AGGAG | AAGAA 11111 AAGAA 11111 AAGAA 1880 CATGT | GATGC 11111 GATGC 11111 GATGC GTTGC | TCGAG TCGAG 11111 TCGAG 11111 TCGAG 1890 CTATG | ACTCC ACTCC 11111 ACTCC 11111 ACTCC ATCCC | AGGGC 11111 AGGGC 11111 AGGGC 1900 TAATG | CGTAC 11111 CGTAC 11111 CGTAC 11111 CGTAC | CTCTT 11111 CTCTT 11111 CTCTT 11111 CTCTT 1910 GCTTT | GGATA 11111 GGATA 11111 GGATA CAAGG | TAATC 11111 TAATC 11111 TAATC 1920 ATATG |
| U22/1A B73/7-4 XI12/8A | GTCCG 11111 GTCCG 11111 GTCCG GTCCC | CGCAG CGCAG 11111 CGCAG 11111 CGCAG 1870 ACACC | CGATA 11111 CGATA 11111 CGATA AGGAG AGGAG | AAGAA AAGAA 11111 AAGAA 11111 AAGAA 1880 CATGT | GATGC 11111 GATGC 11111 GATGC GTTGC | TCGAG TCGAG 11111 TCGAG 11111 TCGAG 1890 CTATG | ACTCC ACTCC 11111 ACTCC 11111 ACTCC ATCCC | AGGGC AGGGC 11111 AGGGC 11111 AGGGC 1900 TAATG TAgTG | CGTAC 11111 CGTAC 11111 CGTAC 11111 CGTAC GTGGG | CTCTT 11111 CTCTT 11111 CTCTT 1910 GCTTT | GGATA 11111 GGATA 11111 GGATA CAAGG | TAATC 11111 TAATC 11111 TAATC 11111 TAATC 1920 ATATG |
| W22/1A B73/7-4 X112/8A X112/8A W22/1A | GTCCG 11111 GTCCG 11111 GTCCC GTCCC 11111 | CGCAG CGCAG 11111 CGCAG 11111 CGCAG 1870 ACACC ACACC 11111 | CGATA 11111 CGATA 11111 CGATA AGGAG AGGAG 11111 | AAGAA 11111 AAGAA 11111 AAGAA 1880 CATGT 11111 | GATGC 11111 GATGC 11111 GATGC GTTGC 11111 | TCGAG TCGAG 11111 TCGAG 11111 TCGAG 1890 CTATG CTATG 11111 | ACTCC 11111 ACTCC 11111 ACTCC ATCCC 11111 | AGGGC 11111 AGGGC 11111 AGGGC 1900 TAATG TAGTG 11111 | CGTAC 11111 CGTAC 11111 CGTAC GTGGG GTGGG 11111 | CTCTT 11111 CTCTT 11111 CTCTT 1910 GCTTT GCTTT 11111 | GGATA 11111 GGATA 11111 GGATA CAAGG CAAGG 11111 | TAATC 11111 TAATC 11111 TAATC 1920 ATATG 11111 |
| H22/1A B73/7-4 XI12/8A XI12/8A | GTCCG 11111 GTCCG 11111 GTCCC GTCCC 11111 GTCCC | CGCAG CGCAG 11111 CGCAG 11111 CGCAG 1870 ACACC ACACC 11111 ACACC | CGATA 11111 CGATA 11111 CGATA 11111 CGATA AGGAG AGGAG 11111 AGGAG | AAGAA 11111 AAGAA 11111 AAGAA 11880 CATGT CATGT 11111 CATGT | GATGC 11111 GATGC 11111 GATGC GTTGC 11111 GTTGC | TCGAG TCGAG 11111 TCGAG 11111 TCGAG CTATG 11111 CTATG | ACTCC 11111 ACTCC 11111 ACTCC ATCCC 11111 ATCCC | AGGGC AGGGC 11111 AGGGC 11111 AGGGC 1900 TAATG TAgTG | CGTAC 11111 CGTAC 11111 CGTAC 11111 CGTAC GTGGG 11111 GTGGG | CTCTT 11111 CTCTT 11111 CTCTT 1910 GCTTT 11111 GCTTT | GGATA 11111 GGATA 11111 GGATA CAAGG CAAGG 11111 CAAGG | TAATC 11111 TAATC 11111 TAATC 11111 TAATC ATATG 11111 ATATG |

| | | 1930 | | 1940 | | 1950 | | 1960 | | |
|---------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| XI12/8A | ATCCT | GGATG | GTGAT | GGCAG | GACTG | TGTAC | TGATC | TAAAA | TCCAG | CAAG |
| A55/19 | ATCCT | GGATG | GTGAT | GGCAG | GACTG | TGTAC | TGATC | TAAAA | TCCAG | CAAG) |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 1111 |
| B73/7-4 | ATCCT | GGATG | GTGAT | GGCAG | GACTG | TGTAC | TGATC | TAAAA | TCCAG | CAAG) |
| | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 1111 |
| XI12/8A | ATCCT | GGATG | GTGAT | GGCAG | GACTG | TGTAC | TGATC | TAAAA | TCCAG | CAAG |

FIG.7 I

| | 1 | 0 6 | 20 3 | 10 | 10 | 50 60 |
|---------|-------------|-------------|--------------------------------|--------------|-------------|------------------------------------|
| XI12/8A | MATAA AASTA | LTGAT TAAP | (ARRRA HLLAT | RRALA APIRO | SAASP AMP | MA PPATP LRPYG |
| W22/1A | | | | | | MA PPATP LRPYG |
| B73/7-4 | ATAA AASTA | LTGAT TAAP | (ARRRA HLLAT | RRALA APIR | SAASP AMP | HA PPATP LRPYG |
| XI12/8A | | | | | | 11 11111 11111 MA PPATP LRPYG |
| | 7 | 'O { | 30 9 | in t | 00 | 110 120 |
| XI12/8A | = | - | | | | FR HEQGE AFAAS |
| H22/1A | PTDPR KGADI | | | | - | FR HEQGE AFAAS |
| B73/7-4 | PTePR KGADI | LVESL ERCG | / RDVFA YPGG/ | SMEIH QALTI | SPAIN NHT | FR HEDGE AFAAS |
| XI12/8A | 20 00 00000 | | | | | 11 11111 11111 FR HEQGE AFAAS |
| | 13 | 10 14 | 40 15 | in 1 | 50 | 170 180 |
| X112/8A | | - | | | | MIG TDAFQ ETPIV |
| H22/1A | | | | | | MIG TDAFO ETPIV |
| B73/7-4 | | | | | | 111 11111 11111 MIG TDAFO ETPIV |
| XI12/8A | | | | | | 111 11111 11111 MIG TDAFO ETPIV |
| | | | nn 31 | h 2 | 30 | 220 240 |
| X112/8A | EALK2 ILKH | | | .A SSGRP GPV | | 66W VALAA DKLW2 530 540 |
| #22/1Å | | | | | | OOM AANAA DKIMZ |
| B73/7-4 | | | 11 11111 1111 IP RVVQE AFFU | | | 111 11111 11111 |
| XI12/8A | 11111 1111 | 1 11111 111 | 11 11111 111 | 1 11111 111 | 11 11111 11 | 111 11111 11111 |

| | | 250 | | 260 | | 270 | | 280 | | 290 | | 300 |
|---|--|--|--|---|---|---|---|--|--|--|--|---|
| XI12/8A | LPGYI | ARLPK | PPATE | LTF6A | LRLVG | FZKKh | VLYVG | GGCAA | SGEEL | RRFVE | LTGIP | VIIIL |
| A55/19 | | | | | | | | | | | LTGIP | |
| | | | | | | | | | | | 11111 | |
| B73/7-4 | | | | | | | | | | • • • • • • | LTGIP | |
| W. 10.101 | | | | | | | | | | | 11111 | |
| X112/8A | LPGAT | AKLYK | PPAIL | FFFAA | LKL AP | F2KKh | VLYVU | UULAA | ZUEEL | KKI AF | LTGIP | AIIIL |
| | | 310 | | 320 | | 330 | | 340 | | 350 | | 360 |
| XI12/8A | HGLGN | FPSDD | PLSLR | HLGMH | GTVYA | DVAYD | KADLL | LALGV | RFDDR | ALCKI | EAFAS | RAKIV |
| W22/1A | HCI CN | rasq | PI SI R | MI CWH | GTVYA | NYAVN | KADI I | I AL GV | REDDR | ALUKI | EAFAS | BVKIA |
| WELLY IVI | | | | | | | | | | | 11111 | |
| B73/7-4 | | | | | | | | | | | EAFAS | |
| | | | | | | | | | | | 11111 | |
| XI12/8A | MGLGN | FPSDD | PLSLR | HLGMH | GTVYA | UAAA | KADLL | LALGV | RFDDR | ALCK I | EAFAS | RAKIV |
| | | | | | | | | | | | | |
| | | 270 | | 200 | | 201 | | ANN | | 410 | | ADN |
| V[12/QA | ⊔vnin | 370 PAE16 | KNKOĐ | 380 112VH | VDARI | 990 390 | NALLE | 004 12772 | RCEDE | 410 GSVMD | EI TIOO | 420 VDEED |
| X112/8A | HVDID | | KNKQP | | ADVKL | | NALLE | | KSFDF | _ | ELDQQ | |
| AB\S11X A1\SSU | | PAEIG | | HVSIC | | ALQGH | | GSTSK | | CSAND | ELDQQ ELDQQ | KREFP |
| | HVDID | PAEIG PAEIG | KNKQP | HA21C | ADVKL | ALQGH ALQGM | NALLE | C212K | KSFDF | CZAND CZAND | | KREFP KREFP |
| | HVDID 11111 | PAEIG 11111 | KNKQP 11111 | 11111 HA21C | ADVKL | ALQGM ALQGM 11111 | NALLE 11111 | 0212K | KSFDF 11111 | 11111 G2AND G2AND | ELDQQ | KREFP KREFP 11111 |
| H22/1A | HVDID 11111 HVDID | PAEIG PAEIG 11111 PAEIG | KNKQP 11111 KNKQP | HVSIC 11111 HVSIC | ADVKL 11111 ADVKL | ALQGM ALQGM 11111 ALQGM | NALLE 11111 NALLE | G212K 11111 G212K G212K | KSFDF 11111 KSFDF | CSAND 11111 CSAND CSAND | ELDQQ 11111 | KREFP KREFP 11111 KREFP |
| H22/1A | HVDID 11111 HVDID 11111 | PAEIG 11111 PAEIG 11111 | KNKQP 11111 KNKQP | HVSIC 11111 11111 | ADVKL 11111 ADVKL | ALQGM 11111 ALQGM 11111 | NALLE 11111 NALLE 11111 | 11111 G212K 11111 G212K | KSFDF 11111 KSFDF 11111 | 11111 62AND 11111 62AND G2AND | ELDQQ 11111 ELDQQ | KREFP 11111 KREFP 11111 |
| ₩22/1A B73/7-4 | HVDID 11111 HVDID 11111 | PAEIG PAEIG 11111 PAEIG 11111 PAEIG | KNKQP 11111 KNKQP | HAZIC 11111 HAZIC HAZIC HAZIC | ADVKL 11111 ADVKL | ALOGH ALOGM 11111 ALOGM 11111 ALOGM | NALLE 11111 NALLE 11111 | GSTSK 11111 GSTSK 11111 GSTSK | KSFDF 11111 KSFDF 11111 | CZAND 11111 CZAND 11111 CZAND CZAND | ELDQQ 11111 ELDQQ 11111 | KREFP 11111 KREFP 11111 KREFP |
| ₩22/1A B73/7-4 | HVDID 11111 HVDID 11111 HVDID | PAEIG PAEIG 11111 PAEIG 11111 PAEIG 430 | KNKQP 11111 KNKQP 11111 KNKQP | HVSIC 11111 11111 11111 HVSIC 440 | ADYKL 11111 ADYKL 11111 ADYKL | ALOGH ALOGM 11111 ALOGM 11111 ALOGM 450 | NALLE 11111 NALLE 11111 NALLE | GSTSK GSTSK 11111 GSTSK 11111 GSTSK 460 | KSFDF 11111 KSFDF 11111 KSFDF | GSYND GSYND 11111 GSYND 11111 GSYND | ELDQQ 11111 ELDQQ 11111 | KREFP 11111 KREFP 11111 KREFP 480 |
| H22/1A B73/7-4 XI12/8A XI12/8A | FCAKL HADID 11111 HADID 11111 HADID | PAEIG 11111 PAEIG 11111 PAEIG 430 SNEEI | KNKQP 11111 KNKQP 11111 KNKQP | HVSIC 11111 HVSIC 11111 HVSIC 440 | ADYKL 11111 ADYKL 11111 ADYKL ELTKG | ALOGH ALOGM 11111 ALOGM 11111 ALOGM 450 EATIG | NALLE 111111 NALLE 111111 NALLE | GSTSK GSTSK 11111 GSTSK 11111 GSTSK 460 HQMYA | KSFDF 11111 KSFDF 11111 KSFDF | GSYND GSYND 11111 GSYND 11111 GSYND 470 YKRPR | GAF22 EFDG6 11111 EFDG6 111111 EFDG6 | KREFP 11111 KREFP 11111 KREFP 480 AGLGA |
| H22/1A B73/7-4 XI12/8A | FRANCE FR | PAEIG 11111 PAEIG 11111 PAEIG 430 SNEEI | KNKQP 11111 KNKQP 11111 KNKQP QPQYA | HVSIC 11111 HVSIC 11111 HVSIC 11111 104FD | ADYKL 11111 ADYKL 11111 ADYKL ELTKG | ALOGH ALOGM 11111 ALOGM 11111 ALOGM 450 EATIG | NALLE 11111 NALLE 11111 NALLE TGVGQ | GSTSK GSTSK 11111 GSTSK 11111 GSTSK 460 HQMYA | KSFDF 11111 KSFDF 11111 KSFDF AQYYT | GSHND GSHND 11111 GSHND 11111 GSHND 470 YKRPR | OAF22 OAF22 OAF22 OAF22 | KREFP 11111 KREFP 11111 KREFP 480 AGLGA |
| H22/1A B73/7-4 XI12/8A XI12/8A | FEAKL 11111 HADID 111111 HADID HADID | PAEIG 11111 PAEIG 11111 PAEIG 430 SNEEI SNEEI | KNKQP 11111 KNKQP 11111 KNKQP QPQYA QPQYA 11111 | HVSIC 11111 HVSIC 11111 HVSIC 440 104LD 101111 | ADYKL 11111 ADYKL 11111 ADYKL ELTKG ELTKG | ALOGH ALOGM 11111 ALOGM 11111 ALOGM 450 EATIG 11111 | NALLE 111111 NALLE 111111 NALLE TGVGQ TGVGQ 111111 | GSTSK GSTSK 11111 GSTSK 11111 GSTSK 460 HQMYA HQMYA 11111 | KSFDF 11111 KSFDF 11111 KSFDF AQYYT AQYYT 11111 | GSYND GSYND 11111 GSYND 11111 GSYND 470 YKRPR YKRPR 11111 | 0AF22 0AF22 0AF22 11111 EFD00 111111 EFD00 | KREFP 11111 KREFP 11111 KREFP 480 AGLGA AGLGA 11111 |
| H22/1A B73/7-4 XI12/8A XI12/8A | FRANCE TO THE PROPERTY OF THE | PAEIG 11111 PAEIG 11111 PAEIG 430 SNEEI SNEEI 11111 SNEEI | KNKQP 11111 KNKQP 11111 KNKQP QPQYA QPQYA 11111 QPQYA | HVSIC 11111 HVSIC 11111 HVSIC 440 10VLD 11111 10VLD | ADYKL 11111 ADYKL 11111 ADYKL ELTKG 11111 ELTKG | ALOGH ALOGM 11111 ALOGM 450 EATIG 11111 EATIG | NALLE 11111 NALLE 11111 NALLE TGVGQ 11111 TGVGQ | GSTSK GSTSK 11111 GSTSK 11111 GSTSK 460 HQMYA 11111 HQMYA | KSFDF 11111 KSFDF 11111 KSFDF AQYYT AQYYT 11111 AQYYT | GSHND GSHND 11111 GSHND 11111 GSHND 470 YKRPR 11111 YKRPR | OAF22 0AF22 11111 EFD00 111111 EFD00 | KREFP 11111 KREFP 11111 KREFP 480 AGLGA AGLGA 11111 AGLGA |
| H22/1A B73/7-4 XI12/8A XI12/8A H22/1A | FEAKL TITTE FANDED TO THE FANDED FOR | PAEIG 11111 PAEIG 11111 PAEIG 430 SNEEI 11111 SNEEI 11111 | KNKQP 11111 KNKQP 11111 KNKQP QPQYA QPQYA 11111 QPQYA 11111 | HAZIC 11111 HAZIC 11111 HAZIC 10AFD 10AFD 11111 10AFD | ADYKL 11111 ADYKL 11111 ADYKL ELTKG 11111 ELTKG 11111 | ALOGH ALOGM 11111 ALOGM 11111 ALOGM 450 EATIG 11111 EATIG 11111 | NALLE 11111 NALLE 11111 NALLE TGVGQ 11111 TGVGQ 11111 | GSTSK 11111 GSTSK 11111 GSTSK 460 HQMYA HQMYA 11111 HQMYA 11111 | KSFDF 11111 KSFDF 11111 KSFDF AQYYT AQYYT 11111 AQYYT 11111 | GSYND 11111 GSYND 11111 GSYND 470 YKRPR YKRPR 11111 YKRPR 11111 | 0AF22 0AF22 0AF22 11111 EFD00 111111 EFD00 | KREFP 11111 KREFP 11111 KREFP 480 AGLGA AGLGA 11111 AGLGA 11111 |

| | 490 | 500 | 510 | 520 | 530 | 540 |
|--------------|---------------------|---------------|-------------|-------------|-------------|--------------------|
| XI12/8A | MGFGL PAAAG | ASVAN PGVTV | VDIDG DGSFL | MNVQE LAMIR | IENLP VKVFV | LNNQH LGMVV |
| H25/19 | MGFGL PAAAG | ASVAN PGVTV | VDIDG DGSFL | MNVQE LAMIR | IENLP VKVFV | LNNQH LGMVV |
| | 11111 11111 | 11111 11111 | 11111 11111 | 11111 11111 | 11111 11111 | 11111 11111 |
| B73/7-4 | MGFGL PAAAG | ASVAN PGVTV | VDIDG DGSFL | MNVQE LAMIR | IENLP VKVFV | LNNQH LGMVV |
| | .11111 111111 | 11111 11111 | 11111 11111 | 11111 11111 | 11111 11111 | 11111 11111 |
| XI12/8A | MGFGL PAAAG | ASVAN PGVTV | YDIDG DGSFL | MNVQE LAMIR | IENLP VKVFV | LNNOH LGMVV |
| | | | | | | |
| | 550 | | | 580 | | |
| XI 12/8A | QHEDR FYKAN | RAHTY LGNPE | NESEI YPDFY | TIAKG FNIPA | ABALK KNEAB | AAIKK WLETP |
| | 011770 717/11 | B | | ~**** | | |
| #22/1A | | RAHTY LGNPE | | | | |
| 570 IZ 4 | | 11111 11111 | | | | |
| B73/7-4 | | RAHTY LGNPE | | | | |
| WT 4 G 4 G 4 | | 11111 11111 | | | | |
| XI12/8A | MAFDK LAKWN | RAHTY LGNPE | WEZFI Abaha | ITAKU FNIPA | AKAIK KNEAK | AAIKK MLEIP |
| | /10 | (20 | (20 | | | |
| VI 12/0A | 610 CDVII 1111VD | | | | | |
| XI12/8A | OFFILL DITAR | HOEHA TAWIA | NUUAF KUMIL | אטעטע ואוי | | |
| A55/19 | CDVII NTIVD | HOEHV LPMIP | | DEDED TAXA | | |
| NCC/ IM | | 11111 11111 | | | | |
| B73/7-4 | | HQEHV LPHIP | | ***** | | |
| ו ועוע | | 11111 11111 | 1111 11111 | | | |
| XI12/8A | | HQEHV LPMIP | | | | |
| VIII' NU | OLIFF DITAL | HELITY LITTLE | דנותא אוואר | ו או אטעטע | | |

FIG.8C